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us-ro-092-/50-ra1
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FIT MOV 12 14:34:48 2004

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GENERAL INFORMATION:
APPLICANT: FALB, Dean A.
TITLE OF INVENTUON: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTUON: COMPOSITIONS AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FILE REFERENCE: 7853-126
CURRENT APPLICATION NUMBER: US/09/126,640A
CURRENT FILING DATE: 1990-07-30
EARLIER FILING DATE: 1990-07-08
EARLIER FILING DATE: 1990-07-08
EARLIER FILING DATE: 1997-02-16
EARLIER FILING DATE: 1997-02-16
MUMBER OF SEQ ID NOS: 44
SOFTWARE: FESTSEQ for Windows Version 4.0
SERVING DATE: 1996-02-16
SOFTWARE: PARESEQ for Windows Version 4.0
SERVILER FILING DATE: 1996-02-16
SOFTWARE: PARESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.4%; Score 160; DB 3; Length 283; Best Local Similarity 96.8%; Pred. No. 4.5e-15; Matches 30; Conservative 1; Mismatches 0; Indels
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Patent No. 6221628
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
CARDIOVASCULAR DISEASE
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ZIPTE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: OB COMPUTER:
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CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
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                    Application US/09126640A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 283
TYPE: PRT
CRGANISM: Homo sapiens
US-09-126-640-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-925-588-6
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Fatent No. 6087477
Fatent No. 6087477
FALENERAL INFORMATION:
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CARDIOVASCULAR DISEASE
FURBERS OF SEQUENCES: 44
CORRESSONDENCE ADDRESS:
ADDRESSED: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: NW York
STRATE: Diskette
COUNTRY: USA
ZIP: 10036-ZIP: Diskette
COUNTRY: LOSA
SOFTWARE: Diskette
COUNTRR: Diskette
COUNTRR: Diskette
COUNTRR: STRATE: DOSE
SOFTWARE: FORM:
MEDIOMICA SYSTEM: DOS
SOFTWARE: FASISED Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495
FILLING DATE:
ADDRESSED: DATE: US/08/944,495
                                                                                                                                                                                                                                                                                                                                                                                                                                   74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
                                                                                                                                                                                                                                                                                                                                                                                               2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
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FILING PRICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/799,910,

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-067-999

TELEPHONE: (212)7909090

TELEPHONE: (212)7909090

TELEPHONE: (212)7909090

TELEPHONE: (212)869741

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENOTH: 283 amino acids

TENOTH: 283 amino acids

TOTOLOGY: unknown
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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FRAGMENT TYPE: internal
US-08-944-495-6
                                                                                                                             ; FRAGMENT TY
US-08-826-246-6
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US-08-944-495-6
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US-09-126-640-9
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Gaps

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STRANDEDNESS: unknown

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ch 72.4%; Score 160; DB 4; Length 283; 1 Similarity 96.8%; Pred, No. 4.5e-15; 30; Conservative 1; Mismatches 0; Indels
                                                                                            Length 283;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08825486
; Sequence 6, Application US/08825486
; Patent No. 6534641
; GENERAL INFORMATION:
    APPLICANT: Falb, Dean
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
    TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
    TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
    TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: PENNIE & EDMONDS LLP
    STREET: 1155 Avenue of the Americas
    CITY: NAY
    STREET: NY
                                                                                            Query Match 72.4%; Score 160; DB 4; Best Local Similarity 96.8%; Pred. No. 4.5e-15; Matches 30; Conservative 1; Mismatches 0
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ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFFRATING SYSTEM: DOS
SOFTWARE: FRAESEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 28-MAR-1997
CLASSIFICATION NUMBER: US/08/825,486
FILING DATE: 28-MAR-1997
CLASSIFICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTONNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-077-999
TELERPAN: (212)7909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KWDIDNILGIEISWENKLAEGLKLILDIIFV 32
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US-06-826-248-6
Sequence 6, Application US/08826248
; Patent No. 6759210
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERICSICS:
LENGTH: 283 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
FRAGMENT TYPE: internal
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-372-044-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-825-486-6
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Best Local S:
Matches 30,
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APPLICANT: Dean A. Falb

APPLICANT: Michael Bonovan

APPLICANT: Michael Donovan

APPLICANT: Michael Donovan

APPLICANT: Michael Bonovan

APPLICANT: Michael A. Gimbrone, Jr.

TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of

TITLE OF INVENTION: Cardiovascular Disease

FILE REFERENCE: 7853-140-99

CURRENT APPLICATION NUMBER: US/09/288, 292A

CURRENT FILING DATE: 1997-06-06

PRIOR FILING DATE: 1997-02-13

PRIOR FILING DATE: 1997-02-13

PRIOR FILING DATE: 1997-02-16

PRIOR FILING DATE: 1995-02-16

PRIOR FILING DATE: 1995-02-16

PRIOR FILING DATE: 1995-02-16

PRIOR FILING DATE: 1995-02-10

PRIOR FILING DATE: 1995-02-10

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 283
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Sequence 6, Application US/09372044A

Batent No. 6422126

GENERAL INFORMATION:

The APPLICANT: Dean FALB et al.

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
FILE REFERENCE: 7853-152

CURRENT APPLICATION NUMBER: US/09/372,044A

CURRENT FILING DATE: 1999-08-11

NUMBER OF SEQ ID NOS: 44

SOUTHWARE: FastSEQ for Windows Version 4.0

SEQ ID NO SEQ ID NOS: 44

LENGTH: 283
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                                                                                                                                                                         Query Match 72.4%; Score 160; DB 3; Length 283; Best Local Similarity 96.8%; Pred. No. 4.5e-15; Matches 30; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                           74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
                                                                                                                                                                                                                                                                              2 KWDIDNILGTEISWENKLAEGLKLILDTIFV 32
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       TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-925-588-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09288292A
Patent No. 6359194
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-288-292A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-288-292A-9
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US-09-372-044-6
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Gaps

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Sequence 1344, Application US/09489039A
Sequence 13424, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
PAPPLICAMIT GALY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIBLLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PELING DATE: 2000-01-27
PRIOR PAPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KWDTDNTLGTEISWENKLAEGLKLTLDTIF 31
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,227
FILING DATE: Filed Herewith
PRICA PAPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0135 US
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGIGTRATION NUTWHER: 36,749
REFRENCE/DOCKET NUMBER: 9F-01
TELEFRHONE: 415-85-055
TELEFACMUNICATION INFORMATION:
TELEFACMUNICATION INFORMATION:
TELEFACMUNICATION INFORMATION:
TELEFACMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
LENGHT: 292 annino acids
TYPE: annino acid
TYPE: annino acid
STRANDEDNESS: single
TOPPOLOGY: linear
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHERICAL: NO
ANT. SENSE: NO
FRAGMENT TYPE: N-termina
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBa
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US-09-489-039A-13424
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US-09-886-319A-64
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US-08-726-227-3
(Sequence 3, Application US/08726227)
(Sequence 3, Application US/08726227
(Sequence 3, Application US/0872627
(Sequence 3, Application US/0872627
(Sequence 3, Application US/0872627
(SEQUENCE)
(S
                                    APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

CONDUTRY: 1034

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VERSION 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,248
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
FILING DATE: 16-FEB-1966
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-079-99
TELECHANICATION INDRER: 7853-079-99
TELECHANICATION INDRER: 7853-079-99
TELECHANICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)8699741
TELEX: 66414 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 mino acids
TYPE: amino acid
STRANDEDNESS: unknown
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COMPUTER READABLE FORM:
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        GENERAL INFORMATION:
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Job time : 12.9136 secs

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APPLICANT: Worler, Saking
APPLICANT: Werner, Sabine
APPLICANT: Werner, Sabine
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Halle, Jorn-Peter
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: Use of Polypeptides or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/01402
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/22,081
PRIOR APPLICATION NUMBER: US 60/22,081
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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We obside 192-941

We obside 2941, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 1596-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-01

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CurapatSegFormatter Version 0.9

SEQ ID NO 941

LEAGURE 1822
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24.0%; Score 53; DB 4; Length 822;
Best Local Similarity 37.0%; Pred. No. 49;
Matches 10; Conservative 5; Mismatches 12; Indels
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LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P16591
US-09-38-092-941
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286 ENENLQANEIMWANLTAESLQVMLKTL 312
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Sequence 64, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Search completed: November 10, 2004, 12:32:26

Sequence

Sequence 17, Appl Sequence 68, Appl Sequence 175, Appl Sequence 175, Appl Sequence 17, Appl Sequence 17, Appl Sequence 57, Appl Sequence 57, Appl Sequence 56, Appl Sequence 12, Appl Sequence 1690, Appl Sequence 12, Appl Sequence 11, Appl Sequence 2611, Appl Sequence 2611, Appl Sequence 2611, Appl Sequence 2559, Appl Sequence 2559, Appl Sequence 2559, Appl Sequence 2559, Appl Sequence 25601, Appl Sequen

us-10-092-750-12.rapb

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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US-10-V92-/20-14

US-10-V92-/20-14

Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Hammond, Philip W.

APPLICANT: Mright, Martin C.

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT APPLICATION NUMBER: US 60/274,526

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SEQ ID NO 12

LENGTH: 40

LENGTH: 40
                                                                  US-10-408-765A-68

US-10-408-765A-175

US-10-408-765A-175

US-10-424-599-195196

US-09-930-512-60

US-09-930-512-59

US-09-930-512-58

US-09-930-512-58

US-09-930-512-58

US-09-930-512-58

US-10-408-765A-1690

US-10-408-765A-1690

US-10-408-765A-1690

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US-10-408-765A-1690

US-10-408-765A-1690

US-10-408-765A-1690

US-10-425-115-331399

US-10-425-115-3187

US-10-424-599-260820

US-10-424-599-189192

US-10-424-599-189192

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100.0%; Pred. No. 1.1e-23;
iive 0; Mismatches 0;
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Publication No. US20040058338A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 40; Conservative
  TYPE: PRT; ORGANISM: Homo sapiens
US-10-092-750-12

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  RESULT 2
     8
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Sequence 140, App
Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1254, Ap
Sequence 1427, Ap
Sequence 1427, Ap
Sequence 14, Appl
                                                                                                                                                                 November 10, 2004, 15:53:52; Search time 38.5802 Seconds (without alignments) 366.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2_6/ptodata/1/pubpaa/PtoT PUBCCMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PtoT Waw PUB.pep:*

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221
1 MKWDTDNTLGTEISWENKLAEGLKLTLDTIFVHHVLHAPH 40
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-307-817-140

US-08-825-486-6

US-08-817-644-9

US-09-372-044-6

US-09-372-044-6

US-09-560-150-9

4 US-10-264-049-2654

6 US-10-264-049-2654

6 US-10-408-765A-1427

6 US-10-408-765A-1647

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US-09-981-353-108
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 2000000000
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Match
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18102, A 3325, Ap 260822, 112494, 189192,

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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Gaps

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Indels 40

Length 40;

Score

Result

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APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILLE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT PILLING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSequist version 0.1
SEQ ID NO 140
LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08825486
Publication No. US20020016303A1
GENERAL INFORMATION:
APPLICANT: FALL, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,486
FILING DATE: 28-MAR.1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/799,910
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTE A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7853-077-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-307-817-140
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TELEX: 60
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US-08-825-486-6
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18-Geguence 9, Application US/00870434

18-Geguence 9, Application US/00870434

18-Deblication No. US20020034736A1

GENERAL INFORMATION: TREATWENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

TITLE OF INVENTION: TREATWENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

ITILE OF INVENTION: TREATWENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LIP

STREET: 1155 Avenue of the Americas

CITY: New York

CONTRY: USA

ZIP: 10036/2711

COMPUTER READABLE PORM:

MEDIUM TYPE: DISKette

OFFRATING SYSTEM: DAY

COMPUTER SEABLE OF OFFI

OFFRATING SYSTEM: DAY

COMPUTER SEABLE OFFI

OFFRATION NUMBER: US/08/799, 910

FILING DATE: 06-UN-1997

CLASSIFICATION UNMER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION UNMER: 30,742

REGISTRATION UNMER: 30,742

REGISTRATION UNMER: 30,742

REGISTRATION UNMER: 12-F88-1997

TELEPHONE: 212-869-864

INPORMATION CONTRYSTION:

REGISTRATION PROMER: 30,742

REGISTRATION PROME
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Patent No. US20020102603A1

DEBERRAL INFORMATION:
APPLICANT Dean FALB et al.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease;
PILE REFRENCE: 783-152
CURRENT APPLICATION UNDER: 1999-08-11

CURRENT FILING DATE: 1999-08-11

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 6
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Best Local Similarity 96.8%; Pred. No. 4.8e-14;
Matches 30; Conservative 1; Mismatches 0;
                                        74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
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MOLECULE TYPE: protein
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US-09-372-044-6
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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Matches 30; Conservative
                                                                                                                                                                                            LENGTH: 283
TYPE: PRT
CRGANISM: Homo sapiens
US-10-067-741-9
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; ORGANISM: Homo sapiens
US-10-264-049-2654
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Matches 30; Conserva
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Publication No. US200300730761
; GENERAL INFORMATION:
APPLICANT: FALLS, Dean A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE;
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE;
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE;
CURRENT FILING DATE: 1090-04-28
CURRENT FILING DATE: 1996-07-30
PRIOR PRILING DATE: 1996-07-30
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PRILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-14
PRIOR PRILING DATE: 1997-02-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FaatSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 44
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APPLICANT: Katherine Galvin
APPLICANT: Katherine Galvin
APPLICANT: Michael Donovan
APPLICANT: Michael A. Gimbrone, Jr.
TITLE OF INVENTION: Compositions and Methods for the Treatment and
TITLE OF INVENTION: Cardiovascular Disease
TITLE OF INVENTION: 2adiovascular Disease
TITLE OF INVENTION: Cardiovascular Disease
TITLE OF INVENTION: Disposit OS 2002-0-0-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-13
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                                                                                                                      ; DB 9; Length 283;
4.8e-14;
ches 0; Indels
                                                                                                                                                                                                                                                    Score 160; DB; Pred. No. 4.8e-1; Mismatches
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                                                                                                                      Query Match
Best Local Similarity 96.8%;
Matches 30; Conservative
                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-372-044-6
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ORGANISM: Homo sapiens
LENGTH: 283
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Query Match
53.8%; Score 119; DB 1.
Best Local Similarity 80.6%; Pred. No. 3e-08;
Matches 25; Conservative 3; Mismatches
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            TITLE OF INVENTION: NO. US20040010118A1e1 PT-
FILE REFERENCE: 21402-091
CURRENT APPLICATION NUMBER: US/09/930,512
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,692
PRIOR FILING DATE: 2000-08-16
PRIOR FLING DATE: 2000-08-16
PRIOR PLING DATE: 2000-08-16
PRIOR PLING DATE: 2000-08-16
PRIOR PLING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/225,693
PRIOR PLING DATE: 2000-08-18
PRIOR PLING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/226,336
PRIOR PLING DATE: 2000-08-18
PRIOR PLING DATE: 2000-08-2
PRIOR PLING DATE: 2001-08-2
PRIOR PRING DATE: 2001-08-2
PRIOR PLING DATE: 2001-08-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Bing
APPLICANT: Glason, Bradford W.
PAPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-10-408-765A-1647
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LENGTH: 293
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APPLICANT: Ghost, Sounitra S.
APPLICANT: Ghost, Boin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dalle E.
APPLICANT: Warnock, Dalle E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10 DENTIFIED IN THE MITOCHONDRIAL PROTEOME
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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72.4%; Score 160; DB 16; Length 284;
Best Local Similarity 96.8%; Pred. No. 4.8e-14;
Matches 30; Conservative 1; Mismatches 0; Indels
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Pred. No. 4.8e-14;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                 75 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 105
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                                                                                                                                                                                                                                                         2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3005, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zerhusen, Bryan D
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly
APPLICANT: Spaderna, Steven
APPLICANT: Ragionali, Esha A
APPLICANT: Rastelli, Luca
APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Rumud
APPLICANT: Shimkets, Richard
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Szekeres, Edward S
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.4%;
Best Local Similarity 96.8%;
Matches 30; Conservative
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Gerlach, Vale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-408-765A-3005
                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-408-765A-1427
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LENGTH: 284
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Matches
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MacDougall, John
FINTION: No. US20040010118Alel Proteins and Nucleic Acids Encoding Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 283;
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APPLICANT: Glen, Cary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660089.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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Warner-Lambert Company

85 KWNTDNTLGTEIAIEDQICQGLKLTFDTTF 114

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APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 673
LENGTH: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.7%; Score 112; DB 9; Length 294; 66.7%; Pred. No. 3e-07; Live 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020160382A1 900341CD1
US-09-981-353-108
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               Sequence 108, Application US/09981353
Fatent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION UNMERR: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 108
LENGTH: 294
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50.7%; Score 112; DB 16
Best Local Similarity 66.7%; Pred. No. 3e-07;
Matches 20; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 KWNTDNTLGTEIAIEDQICQGLKLTFDTTF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 673, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S. APPLICANT: Frahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/10205194 Publication No. US20030134301A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-673
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US-10-408-765A-673
US-09-981-353-108
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US-10-205-194-17
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## APPLICANT: Lee, Kevin
## APPLICANT: Lee, Kevin
## APPLICANT: Dixon, Alistair
## APPLICANT: Brooksbank, Robert
## APPLICANT: Brooksbank, Robert
## APPLICANT: Brooksbank, Robert
## APPLICANT: Broncock, Robert
## APPLICANT: Broncock, Robert
## APPLICANT: Discording the properties of the properties o
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Search completed: November 10, 2004, 16:35:48 Job time : 39.5802 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 8.08642 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-12 221 1 MKWDTDNTLGTEISWENKLAEGLKLTLDTIFVHHVLHAPH 40 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	voltage-dependent	voltage-dependent	ondrial por	emmal 1	e-deben	fruit	etical prot	cinnamyl-alcohol d	e lipopro	Ę	z	n	hypothetical prote	conserved hypothet	protoporphyrin IX	component of type	oxi	eat	al	oligo-1,6-glucosid	protein-tyrosine k	hypothetical prote	hypothetical prote	ਲ		н	н	ical prot	_
SUMMARIES	Ð	B44422	A38102	A45972	A36875	MMHUP3	865537	T29355	T05413	S73995	A86311	MMNCP	H95307	S72806	E87053	F69189	AE3248	T34594	T40614	G96595	G84012	TVHUFE	T10679	1067	B87020	1AG5	8201	810	290	6293
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ф	Query		50.7	。	50.5	ö		39.8	Ġ	25.8	'n.	24.9	4.	24.4	24.4	24.4	4	4	24.2	4	4	4	4	4	e.	ω,	23.8	ä	m	e.
	Score	11	Н	ч	111	H	6 0	88	53	57	56	55	54.5	54	54	54	ω.	ω.	53.5	'n	53	53	53	53	'n	ď	52.5	ď	ď	ď
	Result No.	Н	~	٣	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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Query Match 50.7%; Score 112; DB 1; Length 295; Best Local Similarity 66.7%; Pred. No. 2.4e-07; Matches 20; Conservative 6; Mismatches 4; Indels

ribonuclease (impo DNA binding protei	regulatory factor hypothetical prote	conserved hypothet hypothetical prote	pullulanase - Ther	hypothetical prote glutamate-cysteine	conserved hypothet	Arsenate reductase	conserved hypothet	hypothetical prote	hypothetical prote	UDP-N-acetylglucos
F86742 A55926	A35913 E81192	AB3111 B98176	S27545	G64164 A35015	A95022	E97893	F69186	T20486	F71006	A64182
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817 963	979	302	1203	286	132	132	234	287	333	424
23.8	23.8	23.5	23.5	23.3	23.1	23.1	23.1	23.1	23.1	23.1
52.5	52.5 52	0 0 0 7 0 7	25	51.5 51.5	21	51	21	51	51	51
30	33 33	34 35	36	37 38	39	0 7	1.2	43	44	45

ALIGNMENTS

RESULT 1	
B44422 voltage-dependent anion channel VDAC2 - human	
C.Species: homo sapiens (man) C.Spate: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999 C.Accession: R44422	-Aug-1999
; Zambronicz, E.B.; Yu, W.H.; Adams, V.; McCabe, E.R.;	
phor. Chem. 2007, 1833-1041, 1839 itle: Cloning and functional expression in yeast of two human isoforms eference number: A44422; MUID:93131931; PMID:8420959	soforms of the outer my
A; Accession: B44422 A; Status: not compared with conceptual translation	
A;Rosidues: 1.294 (BLA> A;Rosidues: 1.294 (BLA> A;Cross-references: GB:L06328; NID:g340200; PIDN:AAB59457.1; PID:g340201	340201
A;Experimental source: liver A;Note: sequence extracted from NCBI backbone (NCBIP:122924) C;Genetics:	
A;Gene: GDB:VDAC2 A;Cross-references: GDB:138281 A;Map position: Xq13-Xq21	
C;Superfamily: porin	
Query Match 50.7%; Score 112; DB 2; Length 294; Best Local Similarity 66.7%; Pred. No. 2.3e-07; Matches 20; Conservative 6; Mismatches 4; Indels 0; Gaps	
Qy 2 KWDIDNILGTEISWENKLAEGLKLTLDTIF 31	
Db 85 KWNTDNTLGTEIAIEDQICQGLKLTFDTTF 114	
RESULT 2 A38102 Avoltane Amandant amion channel-like protein - rat	
	-Jul-2004
C;Accession: A38102 R;Burcau, M.H.; Khrestchatisky, M.; Heeren, M.A.; Zambrowicz, E.B.; Kim, H.	; Kim, H.; Grisar, T.M
O. Elli. Chem. 20., 20.7.2028. 1322 A. Title: Isolation and cloning of a voltage-dependent anion channel-like M-r. A;Reference number: A38102; MUID:92235102; PMID:1373732	1-like M-r 36,000 polyr
A; Accession: A38102 A; Status: preliminary; not compared with conceptual translation	
A, Molecule type: mRNA A, Residues: 1.295 < BUR> A, Cross-references: UNIPROT: P81155	
C, Superfamily: porin	

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Cispecies: Drosophila melanogaster)
Cispecies: Drosophila melanogaster
Cispecies: Dros
                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIP:122926)
R;Kayesr, H.; Kratzin, H.D.; Thinnes, F.P.; Goetz, H.; Schmidt, W.E.; Eckart, K.; Hilschn
Biol. Chem. Hoppe-Seyler 370, 1265-1278, 1989
A;Title: To the Knowledge of human porins. II. Characterization and primary structure of A;Reference number: S07478; MUID:90148194; PMID:2559745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: protein
A.Residues: 2-283 <KAY>
A.Residues: 2-283 <KAY>
A.Residues: 2-283 <KAY>
A.Rote: article in German with English abstract
B.Jotergens, L.; Ilsemann, P.; Kratzin, H.D.; Hesse, D.; Eckart, K.; Thinnes, F.P.; Hilsch
Biol. Chem. Hoppe-Seyler 372, 455-463, 1991
Biol. Chem. Hoppe-Seyler 372, 455-463, 1991
A.Fitle: Studies on human porin. IV. The primary structures of "Porin 31HM" purified from A.Reference number: S16195; MUID:92029673; PMID:1657034
                                                                                    A,Cross-references: UNIPROT:P21796, GB:L06132, NID:g340198, PIDN:AAA61272.1, PID:g340199
A,Experimental source: B cell line WIL-ZNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: acetylated amino end; mitochondrial outer membrane F_12-283/Product: voltage-dependent anion channel 1 #status experimental <MAT> F_12/Nodified site: acetylated amino end (Ala) (in mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A;Molecule type: protein
A;Residues: 2-283 «FPH>
R;Kesidues: 2-283 «FPH>
R;Kesidues: 0.283 «FPH>
R;Kesidues: 2-283 «FPH>
R;Kesidues: 2-283 «FPH>
R;Kesidues: 2-283 «FPH>
R;Kesidues: 2-283 «FPH>
A;Reference number: S04018
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40.3%; Score 89; DB 2; Length 280
Best Local Similarity 59.3%; Pred. No. 0.00028;
Matches 16; Conservative 8; Mismatches 3; Indels
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C,Superfamily: porin
C,Keywords: mitrondrion
F,2-280/Product: porin #status experimental <MAT>
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A;Residues: 1-280 <MES>
A;Cross-references: EMBL:X92408
A;A;Accession: S65506
A;Molecule type: protein
A;Residues: 2-10 <MEW>
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A;Molecule type: mRNA
A;Residues: 1-283 <BLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                mitochondrial porin, long form - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A45972
R;Ha, H.; Hajek, P.; Bedwell, D.M.; Burrows, P.D.
T;Ha, H.; Hajek, P.; Bedwell, D.M.; Burrows, P.D.
A;Biol. Chem. 268, 12143-12149, 1993
A;Title: A mitochondrial porin cDNA predicts the existence of multiple human porins.
A;Reference number: A45972
A;Accession: A4497
A;Accession: A44972
A;Accession: A44972
A;Accession: A44972
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N;Alternate names: 31K porin, lymphocyte; mitochondrial porin 1; porin 31HL; porin 31HM
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A44422; S07478; S16195; S04018
R;Blachly-Dyson, E.; Zambronicz, E.B.; Yu, W.H.; Adams, V.; McCabe, E.R.; Adelman, J.; C
Biol. Chem. 268, 1835-1841, 1993
A;Title: Cloning and functional expression in yeast of two human isoforms of the outer m
A;Reference number: A44422; MUID:93131931; PMID:8420959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-282 <DER>
A,A;Cross-references: UNIPROT:P45879; GB:X75068; NID:g437026; PIDN:CAA52962.1; PID:g437027
C;Superfamily: porin
C;Keywords: voltage-gated ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P45880; GB:LUU8686; vui
C;Superfamily: porin
C;Keywords: alternative initiators; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 KWNTDNTLGTEIAIEDQICQGLKLTFDTTF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 KWNTDNTLGTEIAIEDQICQGLKLTFDTTF 115
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Rimeologis, A.; Etker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Hitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Jate: 3.1 Dec.1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S07195
R;Kleene, R.; Pfanner, N.; Pfaller, R.; Link, T.A.; Sebald, W.; Neupert, W.; Tropschug, N
EMBO J. 6, 2657-2653, 1987
A;Title: Mitochondrial porin of Neurospora crassa: cDNA cloning, in vitro expression and
A;Reference number: S07195; MUID:88054957; PMID:2960519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P75583; EMBL:AE000062; GB:U00089; NID:g1674373; PIDN:AAB96317
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
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C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 873995
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Rwindielc Ascids Ree. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae. A;Reference number: S73395
A;Accession: S73995
A;Accession: S73995
A;Etus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA,
A;Residues: 1-320 cHMA>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86311
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C;Superfamily: Mycoplasma pneumoniae probable lipoprotein VXpSPT7_orf320
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Pred. No. 74;
9; Mismatches 11; Indels
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Best Local Similarity 28.6%;
Matches 16; Conservative 5
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A;Molecule type: DNA
A;Residues: 1-1908 <STO>
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Matches
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A; Residues: 1-357 < BEV>
A; Residues: 1-357 < BEV>
A; Cross-references: UNIPROT:049482; EMBL:AL021961 A; Experimental source: cultivar Columbia; BAC clone F28A23 Cigenetics:
                                                                                                                                                                            RESULT 7
T29355
hypothetical protein R05G6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T29355
R;Murray, J; Le, TT.
Submitted to the EMBL Data Library, May 1996
A,Poscription: The sequence of C. elegans cosmid R05G6.
A,Reference number: Z20612
A;Reference number: Z20612
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T29355
A;Retues: Tpreliminary; translated from GB/EMBL/DDBJ
A;Rocession: ESPECHIBER A;References: EMBL:U58746; PIDN:AAB00622.1; GSPDB:GN00022; CESP:R05G6.7
A;Residues: 1310 cMUR>
A;Residues: ESP:R05G6.7
A;Reperimental source: strain Bristol N2; clone R05G6
C;Genetics:
A;Genetics:
A;Genetics:
A;Hutrons: 22/1; 69/1; 152/3; 238/3
C;Superfamily: porin
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AjIntrons: 30/2; 68/2; 144/2; 291/1
AjIntrons: 30/2; 68/2; 144/2; 291/1
AjIntrons: 30/2; 68/2; 144/2; 291/1
AjNote: F28A2310
CjSuperfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
CjSuperfamily: alcohol dehydrogenase; zinc
Fj32-340,Domain: long-chain alcohol dehydrogenase homology <LAD>
Fj32-340,Domain: long-cha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.8%; Score 88; DB 2; I Best Local Similarity 46.2%; Pred. No. 0.00043; Matches 18; Conservative 6; Mismatches 9;
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Gaps

5

Length 201; Indels

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protogorphyrin IX magnesium chelatase (BC 4.99.1.-) - Methanobacterium thermoautotrophicu ():Species: Methanobacterium thermoautotrophicum ():Species: Methanobacterium thermoautotrophicum ():Species: Methanobacterium thermoautotrophicum ():Species: Methanobacterium thermoautotrophicum ():Species: Methanobacterium ():Species: Methanobacterium ():Species: Methanobacterium ():Species: Methanobacterium thermoautotrophicum ():Species: Methanobacterium thermoautotrophicum Delta H: functi A;Reference number: A69000; MulD:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87053
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R; Cole, S.T.; Eiglmeier, K.M.
Duther, B.M.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-220 <STO>
A, Cross-references: UNIPROT: P53524; GB: AL450380; NID: g13093134; PIDN: CAC31536.1; GSPDB:GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein ML1155 [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 2; Length 220;
Pred. No. 11;
8; Mismatches 10; Indels
                            DB . 7;
                                                                                                           8; Mismatches
                                                                                                                                                                                         3 WDTDNTLGTEISW--ENKLAEGLKLTLDTI 30
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                                     Score 54;
Pred. No.
                                         24.4%;
33.3%;
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llarity 33.3%;
Conservative 8
                                     Query Match
Best Local Similarity 33.3
Matches 10; Conservative
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Best Local Similarity
Local 12; Conserva'
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: E87053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ML1155
                                                                                                                                                                                                                                                                        52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arginine deiminase (BC 3.5.3.6) ArcB [imported] - Sinorhizobium meliloti (strain 1021) m C; Species: Sinorhizobium meliloti (CjDate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Accession: H95307 B; Bearnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. A; Mall, Acc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001 A; Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Recession: H95307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,GESGIGHES: 1-334 < KUNN-
A,GESGIGHES: 1-334 < KUNN-
A,GESGIGHES: 1-334 < KUNN-
A,GESGIGHES: 1-334 < KUNN-
A,GENERATE, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Canie, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones T.
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Rebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A966039; MuID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C;Keywords: hydrolase
                                     A;Residues 1-283 «KLE»
A;Cross-references: UNIPROT:P07144; EMBL:X05824; NID:g3056; PIDN:CAA29264.1; PID:g3057
C;Superfamily: porin
C;Keywords: membrane protein; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein B1549_C3_223 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: J9-Mar-1997 #text_change 23-Mar-2001
C;Accession: S72806
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1549.
A;Reference number: S72886
A;Accession: S72806
A;Accession: S72806
A;Accession: S72806
A;Molecule type: DNA
A;Residues: 1-201 cSML>
A;Accession: C;Cserences: EMBL:U00014; NID:g466903; PIDN:AAA50894.1; PID:g466919
C;Genetics:
A;Actact codon: GTG
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                                                                                                                                                                                                                               Length 283;
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                                                                                                                                                                                                                                                                                                                 7; Indels
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                                                                                                                                                                                                                               24.9%; Score 55; DB 45.5%; Pred. No. 11; ive 5; Mismatches
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24.7%; Score 54.5; E
Best Local Similarity 39.3%; Pred. No. 15;
Matches 11; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 DTETTIGKOISDDYGMSDGLEVT-DEVF 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 10; Conser
A; Molecule type: mRNA
                                                                                                                                                                                                                                       Query Match
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Gaps

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1708 <MTH> A;Residues: 1-1708 <MTH> A;Residues: 1-1708 <MTH> A;Residues: 1-1708 <MTH> A;Experimental source: strain Delta H
                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                         A;Gene: MTH673
C;Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis
C;Keywords: lyase
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                               Length 1708;
                                                                                                                                                                                                                                                                               24.4%; Score 54; DB 2; Length 17C
44.4%; Pred. No. 1.2e+02;
tive 6; Mismatches 7; Indels
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Job time : 10.0864 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 11:27:01; Search time 43.7654 Seconds (without alignments) 525.871 Million cell updates/sec

Run on:

US-10-092-750-12 221 1 MKWDTDNTLGTEISWENKLAEGLKLTLDTIFVHYVLHAPH 40

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cripti	Q9g129 bos taurus	Q9mz13 bos taurus	Q9y277 homo sapien	யாக ய	Q8bng2 mus musculu	Q9r1z0 rattus norv	œ	Q9tt13 oryctolagus		_		~	xenopus la	Q8awd0 brachydanio	Q9i9dl gallus gall		Aah62525 brachydan	homo sa	Q7zwz0 xenopus lae	Cag33245 homo sapi	Q9tt14 oryctolagus	Q9bwk8 homo sapien		Q9mz15 sus scrofa	Aah00165 homo sapi	Aah72407 homo sapi		P81155 rattus norv	_	9 mus	P45880 homo sapien
SUMMAKLES	QI	Q9GL29	POR3 BOVIN	POR3_HUMAN	POR3 MOUSE	Q8BNG2	POR3_RAT	AAH61780	POR3_RABIT	Q9MZ14	POR3_PIG	Q6GR11	POR2 MELGA	POR2_XENLA	QBAWDO	Q919D1	œ	AAH62525	Q713J5	Q7ZWZ0		POR2_RABIT	Q9BWK8	Q9MYV7	Q9MZ15	AAH00165	AAH72407	POR2 MOUSE	POR2_RAT	Q991 <u>9</u> 8	AAQ01516	POR2_HUMAN
	ength DB	. 80	83	83	83	84	83	83	83	83	12	83	82	82	83	83	83	83	83	83	83	94	40	46	46	94	46	95	95	295 2	S S	47
de	Query Match Length	72.4	72.4	72.4	72.4		71.0	71.0	66.5	66.5	63.8	9.95	52.0	52.0	52.0	52.0	52.0	52.0	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7
	Score	160	160	160	160	160	157	157	147	147	141	125	115	115	115	115	115	115	112	112	112	112	112	112	112	112	112	112	112	112	112	112
	Result No.	1	7	m	4	D.	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

P45879 bos taurus P21796 homo sapien	Q9tt15 oryctolagus Q9z2l0 rattus norv	Q71sw7 bos taurus Q9mz16 sus scrofa	Aaf80101 bos tauru	Q60932 mus musculu	Q6p9w9 rattus norv	Aah60558 rattus no	Q6in28 rattus norv	Q9ia66 squalus aca	Q6nwcl brachydanio	Aaq97862 brachydan
POR1_BOVIN POR1_HUMAN	POR1_RABIT POR1_RAT	<u>0718</u> 7 09M216	AAF80101	POR1 MOUSE	Q6P9 <u>W</u> 9	AAH60558	Q6IN28	Q9IA66	Q6NWC1	AAQ97862
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282	282	283 283	283	296	297	297	299	283	283	283
50.2	50.2	50.2	50.2	50.2	50.2	50.2	50.2	49.8	49.3	49.3
111	111	111	111	111	111	111	111	110	109	109
33	3.4 3.5	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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IsoId=Q9Y277-1; Sequence=Displayed;
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MEDLINE=20295349; PubMed=10833333;
Decker W.K., Craigen W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mamm. Genome 10:1041-1042(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                         "Ion channels in the lens.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBU databases.
-!-FUNCTION: Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules (By similarity).
-!-SUBCELGULAR LOCATION: Outer mitochondrial membrane.
-!- DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.
-!- SUMILARITY: Belongs to the eukaryotic mitochondrial porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Unition cord blood;

MEDLINE=98318631; PubMed=9653160;

MAO M., Pu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,

Mao M., Pu G. S.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,

Wang Y.-X., Chen S.-J., Chen Z.;

"Identification of genes expressed in human CD34(+) hematopoietic

stem/progenitor cells by expressed sequence tags and efficient full-
length CDNA cloning.";

Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3)
(Outer mitochondrial membrane protein porin 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rahmani Z., Maunoury C., Siddiqui A., "Isolation of a novel human voltage-dependent anion channel gene."; Eur. J. Hum. Genet. 6:337-340(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
Mitochondrion; Outer membrane; Porin.
SEQUENCE 283 AA; 30739 MW; D305DA2EE42BEC3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160; DB 1;
Pred. No. 6.7e-13;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF268466; AAF80103.1; -.
InterPro; IPRO01925; Porin_Buk.
Pfam, PPO1459; Porin 3, 1.
PRINTS; PR00185; EUKÄRYTPORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
[1]
SEQUENCE FROM N.A.
TISSUE=Lens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29Y277; Q9UISO;
16-OCT-2001 (Re-
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09Y277; 09UI
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                                                                       Rae J.L.;
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POR3 HUMA
POR3 HUMA
POR3 HUMA
POR3 HUMA
POR OOC
POT O
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Xiausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Expleton M., Soars M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

RA Expleton M., Soars M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

RA Bras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabas S.A., McEwan P.J., McKernan K.J., Malke J.A., Gunarane P.H.,

Rabas S.A., McWany D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rabas S.A., Mullan D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabas S.A., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

Rabaseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A., Schmutz J., Whers R.M.,

Rodriguez A., Schmutz J., Whers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A., Schmutz J., Warra 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The tissue-specific, alternatively spliced single ATG exon of the type 3 voltage-dependent anion channel gene does not create a truncated protein isoform in vivo.";
Mol. Genet. Metab. 70:69-74(2000)
-!- FUNCTION: Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:12674; VDAC3.
Genew; HGNC:12674; VDAC3.
GO; GO:0005741; C:mitochondrial outer membrane; TAS.
GO; GO:0015853; F:voltage-dependent anion channel porin activity; TAS.
GO; GO:0015853; F:voltage-dependent ransport; TAS.
HITGETPO: IPRO01925; Porin Euk.
Pfam; PF01459; Porin 3: 1.
PRINTS; PR00185; EUKÄRYTPORIN.
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--- TISSUB SPECIFICITY: Widely expressed. Highest in testis.
--- DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.
--- SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE OF 1-253 FROM N.A. MEDLINE-99431679; PubMed-10501981; MEDLINE-99431679; PubMed-10501981; Scharte E.C., Towbin J.A., Craigen W.J.; Pecker W.K., Bowles K.R., Scharte E.C., Towbin J.A., Craigen W.J.; IREVISEd fine mapping of the human voltage-dependent anion channel loci by radiation hybrid analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
Alternative splicing; Mitochondrion; Outer membrane; Porin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.

STRAIN=FVBD/N; TISSUE=Nammary gland;

MIDINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Fonaldo M.F., Carvinci P., Prange C.

A Rapleton M., Soares M.B., Bonaldo M.F., Carvinci P., Prange C.

A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Roak S.A., McKwan P.J., McKernan K.J., Mark J.L., Gunbarate P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gapk L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gabbs R.A.,

Rhiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schnertch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Schnerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,

B Shinerch A., Schah J.E., Jones S.J.M., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane
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DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.
SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
voltage-dependent anion-selective channel protein 3 (VDAC-3) (mVDAC3)
(Outer mitochondrial membrane protein porin 3).
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sampson M.J., Lovell R.S., Davison D.B., Craigen W.J.; "A novel mouse mitochondrial voltage-dependent anion channel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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SUBCELLULAR LOCATION: Outer mitochondrial membrane.
TISSUE SPECIPICITY: Highest levels of expression detected in testis, less but still abundant expression in heart, Kidney, testis, less but still abundant
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0
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                                                                                                          Length 283;
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-!- FUNCTION: Forms a channel through the mitochondrial o that allows diffusion of small hydrophilic molecules
                                                                                                                                                            0; Indels
39 39 V -> VM (in isoform 2).
/FTId=VSP 005079.
283 AA; 30658 MW; E03CBCEDA72A9783 CRC64;
                                                                                                       72.4%; Score 160; DB 1; 96.8%; Pred. No. 6.7e-13; ive 1; Mismatches 0
                                                                                                                                                                                                                                          2 KWDIDNILGTEISWENKLAEGLKLILDTIFV 32
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                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         localizes to chromosome 8.";
Genomics 36:192-196(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                Local Similarity
ses 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Vdac3;
                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                     SEQUENCE
  VARSPLIC
                                                                                                       Query Match
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060931
                                                                                                                                                                                                                                                                                                                                                                        POR3_MOUSE
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removed. Usage by and for commercial or (See http://www.isb-sib.ch/announce/
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:D130008N07 product:voltage-dependent anion
channel 3, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
The FANYOM CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                      EMBL; U30839; AAB47776.1; -.

REMBL; BC004743; AAB47776.1; -.

RGO; MG: 0001662; P: Dehavioral fear response; IMP.

RGO; GO: 0007612; P: Dehavioral fear response; IMP.

RGO; GO: 0007612; P: Dehavioral fear response; IMP.

RGO; GO: 0007612; P: Dearning; IMP.

RGO; GO: 0007612; P: Dearning; IMP.

RGO; GO: 0007612; P: Dearning; IMP.

R Pfam; PF01459; Porin 3; 1.

R PROSITE; PS00558; BUKARYPORIN; 1.

MICOCHONIATION; OULCET MEMBYRANG; PORIN; 1.

MICOCHONIATION; OULCET MEMBYRANG; PORIN.

SEQUENCE 283 AA; 30753 MW; A95AFD67C611228C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.4%; Score 160; DB 1; Le 96.8%; Pred. No. 6.7e-13; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Spinal ganglion; MEDLINE=99279253; Pubmed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol, 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 KWNTDNTLGTEISWENKLAEGLKLTLDTIFV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 AA.
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   modified and this statement is not remove
entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Spinal gan
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Spinal gan
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 96.8
es 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8BNG2
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Matches
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Rae J.L.; "Ion channels in the lens."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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       ઠ
                                                                                                                                                                                                                                                                                                                                                           Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W., A Hayashida K., Hayasau T., Hirozane T., A Hayashida K., Ishimi Y., Itch M., Kagawa T., Hirozane T., Rabin K., Indian Y., Sondo S., Konno H., Kouda M., Koya S., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Ruihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Rasaki K., Numara K., Numazaki R., Shiraki T., Sogabe Y., Tagami M., Rasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tanaka T., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

EMBL, AKOS176; P. Pebavical fear response; IMP.

GO: GO:0005739; C:mitochondrion; IDA.

GO: GO:0001662; P. Pebavical fear response; IMP.

InterPro; IPRO01955; Porin Buk.

PRINTS; PRO01859; Porin Buk.

PRINTS; PRO185; Porin Buk.

PRINTS; PRO01859; Porin Buk.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRIZO; QSESR2; QSJI31; QSWTU2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (rVDAC3)
(Outer mitochondrial membrane protein porin 3).
SEQUENCE FROM N.A.

STRAIM-CSTBL/60; TISSUE-Spinal ganglion;
MEDLINE=20530913; PLOMMC=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shonno H., Akiyama J., Nishi K., Xitsunai T., Tashinc H., Itoh M., Sumamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tazwa M., Ohara B., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Taraka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., FRIZBN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000)
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MEDLINE-20453129; PubMed-10998068;
Shinohara Y., Ishida T., Hino M., Yamazaki N., Baba Y., Terada H.;
"Characterization of porin isoforms expressed in tumor cells.",
Eur. J. Biochem. 267:6067-6073 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.4%; Score 160; DB 2; Length 284; 96.8%; Pred. No. 6.8e-13; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00558; BUKARYOTIC PORIN; 1.
SEQUENCE 284 AA; 30885 MW; 63B6AA47E4AAC4C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KWDIDNTLGTEISWENKLAEGLKLTLDTIFV 32
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SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 96.8
les 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Vdac3;
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POR3 RAT
LD GORIZO 09
DT GORIZO 09
DT 16-0CT-200
DT 05-JUL-200
DE VOLTAGE-60
DE VOLTAGE-60
DE VOLTAGE-60
DE NAME-VACCE
DE NAME-VACCE
DE NAME-VACCE
DE NAME-VACCE
DE NAME-VACCE
DE NAME-VACCE
DE NAME-113
CON NCBI-TAXIIR
RP SEQUENCE F
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Best Local &
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kidney.

-1- DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.
-1- SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                               Ventura-Clapier R.; very corn isoforms: cloning of a cardiac type-3 variant encoding an additional methionine at its putative N-terminal region."; anophys. Acta 1399:47-50(1998).
Blochim. Biophys. Acta 1399:47-50(1998).
-! FUNCTION: Forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th strong in brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=098120-1; Sequence=Displayed;
Name=2; Synonyms=RVDAC3V;
Isold=098120-2; Sequence=VSP 005080;
-!- TISSUE SPECIFICITY: Isoform I is widely expressed with strong expression in arrium and ascitic tumor, lower levels in brain very low levels in liver and kidney. Isoform 2 is also widely expressed with highest levels in brain but no expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH61780 PRELIMINARY, PRT, 283 AA.
AAH61780,
14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Mitochondrial voltage dependent anion channel 3.
Rattus norvegicus (Ral.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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EMBL; AP268659; AAD22722.1; -.
EMBL; AF048829; AAD22722.1; -.
EMBL; AF048829; AAD22723.1; -.
EMBL; AF048830; AAD22723.1; -.
EMBL; AF048830; AAD22723.1; -.
EMBL; AF048830; AAD2723.1; -.
EMBL; AF048830; AB0373.1; -.
EMBL; BR01959; FORIN_3; 1.
FRINTS; PR01959; FORMARYOTIC_PORIN; 1.
FROMFIF PR00558; EUKARYOTIC_PORIN; 1.
ALTERATIVE SPLICATION (1 isoform 2) ..
VARSPLIC 39 / --
VARSPLIC 128 / --
CONFLICT 128 / --
SEQUENCE 283 AA; 30798 MW; 38002466B6557864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.0%; Score 157; DB 1; Length 283; Best Local Similarity 93.5%; Pred. No. 1.7e-12; Matches 29; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULÂR LOCATION: Outer mitochondrial membrane.

-1- ALTERNATIVE PRODUCTS:

Eventa-Alternative splining; Named isoforms=2;

Name=1; Synonyms=RVDAC3;
                                                                  TISSUE=Heart;
MEDLINE=98390268; PubMed=9714728;
Anflous K., Blondel O., Bernard A., Khrestchatisky M.,
[3] SEQUENCE OF 10-283 FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 KWNIDNTLGTEISWENKLAEGLKLTVDTIFV 104
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ID AAH6
AC AAH6
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Name=VDAC3
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ID _POR3 PIG
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Q9MZ14
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Transperg R.L., Felngold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wann J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peerers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villaion D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willain M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Schwertz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Outer mitochondrial membrane.
DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.
SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
Voltage-dependent anion-selective channel protein 3 (VDAC-3) (Outer mitochondrial membrane protein porin 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 1.7e-12;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Prostate;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO61780; ARH61780.1; -.
SEQUENCE 283 AA; 30784 MW; 3807231491755831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Cornea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%;
llarity 93.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Best Local 29; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=VDAC3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POR3 RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rae J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
POR3_RABET
10
POR3_RABET
116-OCT
DT 16-OCT
DT 16-OCT
DT 05-JUL
DB Voltag
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF268463; AAF78965.1; -. GO; GO:0005741; C:mitochondrial outer membrane; IEA.
GO; GO:0008308; F:voltage-dependent ion-selective channel act. . .; IEA.
GO; GO:0008309; F:voltage-dependent ion-selective channel act. . .; IEA.
GO; GO:000820; P:nnion transport; IEA.
Interpro; IPR001925; Porin Euk.
Pfam; PF01459; Porin 3; 1.
PROMITS; PR001658; EUKARYPORIN.
SEQUENCE 283 AA; 30577 NW; 88CED978CBB45210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
voltage-dependent anion-selective channel protein 3 (VDAC-3)
mitochondrial membrane protein porin 3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.5%; Score 147; DB 1; Length 283; Best Local Similarity 93.5%; Pred. No. 3.7e-11; Matches 29; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 283;
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Best Local Similarity 93.5%; Pred. No. 3.7e-11;
Matches 29; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rae J.L.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        EMBL; AF209727; AAF22837.1; -.
INCEPPO; IPRO1925; PORIN_EUK.
PERM: PRO1459, PORIN_3; 1.
PRINTS; PR00185; EUKÄRYTPORIN.
PROSITE; PS00558; EUKARYOTIC, PORIN; 1.
Mitcchondrion; Outer membrane; Porin.
SEQUENCE 283 AA; 30651 WW; BC0C5616366090A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Voltage-dependent anion channel 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 KWNTDNTLGTEISLENKLAEGLKLTLDTIFV 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                          initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Matches
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                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENRL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                 Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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112 AA; 12126 MW; 23082D5D4811593F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 141; DB 1; L
Pred. No. 8.5e-11;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; F14590; CAA23141.1; -..
InterPro; IPR001925; Porin Buk.
Pfam; PF01459; Porin 3; 1.
PRINTS; PR00185; EUKÄRYTPORIN.
PROSITE; PS00558; EUKÄRYOTIC PORIN; PARTIAL.
NON_TER 1
1 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 63.8%;
1 Similarity 90.3%;
28; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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Q6GR11
ID Q6GR11
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Matches
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (Outer mitochondrial membrane protein porin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
NCBI_TaxID=9103;
                    Clifton S.W.,
                                                        Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                 Klein S., Strausberg R.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC071123; AAH71123.1; -. InterPro; IPR001925; Porin_Euk. Pfam; PF04159; Porin_3; 1. PRINTS; PR00185; EUKÄRYTPORIN. PROSITE; PR00586; EUKÄRYTPORIN. 1. PROCHELical protein.
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                 al protein.
283 AA; 30148 MW; 09EFF65765FA7918 CRC64;
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88ECCF19ABCA004F CRC64;
                  Klein S.L., Strausberg R.L., Wagner L., Pontius J.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                     56.6%; Score 125; DB 2; L
74.2%; Pred. No. 3.2e-08;
ive 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patch 52.0%; Score 115; DB 1; Local Similarity 70.0%; Pred. No. 7e-07; Local 21; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-acetylalanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 KWNTDNTLGTEVALEDKLAKGLKLSLDTTFV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KWDTDNTLGTEISWENKLAEGLKLTLDTIFV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meleagris gallopavo (Common turkey)
MEDLINE=22341132; PubMed=12454917;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.0%; Score 115; DB 2; 70.0%; Pred. No. 7e-07; ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 KWNTDNTLGTEINIEDQIAKGLKLTFDTTF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KWDTDNTLGTEISWENKLAEGLKLTLDTIF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01459; Porin 3; 1. PRINTS; PR00185; EUKARYTPORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L41
SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0919D1;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 70.0
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Whole;
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Matches
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Q919D1
ID Q919D1
AC Q919D1
DT 01-OC
DT 01-OC
      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Krazinh LD, Morris-wortmann C., Schwarzer C., Inlines F.F.,

Hilschmann N.;

The plasma membrane of Xenopus laevis oocytes contains voltage-
T dependent anion-selective porin channels.";

Int. J. Biochem. Cell Biol. 32:225-234(2000)

- FUNCTION: Forms a channel inrough the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. The channel adopts an open conformation at low or zero membrane potential and a closed conformation at low or zero membrane potential and a closed conformation at low or zero membrane potential and a closed conformation at low or zero membrane potential and a closed conformation at low or zero membrane potential and a closed conformation at low or zero membrane potential and a closed conformation at power layour The open state selective [89 similarity).

- I SUNCELLUIAR LOCATION: Outer mitochondrial membrane (Potential).

- I TISSUE SPECIFICITY: Expressed in skeletal muscle and oocytes.

- DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.

- I DOMAIN: Consists mainly of membrane-spanning sided beta-sheets.

- I SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.

- FRINTS; PROO1925; Porin Bux.

- PROSITE; PROO158; EUKARYOTIC_PORIN; 1.

- PROSITE; PROO158; EUKARYOTIC_PORIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-20150664; PubMed-10687956;
Steinacker P., Awni L.A., Becker S., Cole T., Reymann S., Hesse D.,
Kratzin H.D., Morris-Wortmann C., Schwarzer C., Thinnes F.P.,
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craníata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                           н.
Р.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein 2gc:55795 (Voltage-dependent anion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
0
                                                                                                                                                                                                                                                                                                                                                              TISSUBESkeletal muscle;
Reymann S., Kratzin H.D., Hesse D., Hesse J.-O., Klebert S.,
Kiafard Z., Zimmermann B., Spengler B., Metzger S., Thinnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 52.0%; Score 115; DB 1; Length 282; Local Similarity 70.0%; Pred. No. 7e-07; les 21; Conservative 6; Mismatches 3; Indels
                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Voltage-dependent anion-selective channel protein 2 (Outer mitochondrial membrane protein porin).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 1 N-acetylalanine.
282 AA; 30070 MW; B0309215D81FF313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 84-90 AND 274-282, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2).
Name=zgc:55795;
Brachydanio rerio (Zebrafish) (Danio rerio).
73 KWNTDNTLGTEIAIEDQIAKGLKLTFDTTF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KWDTDNTLGTEISWENKLAEGLKLTLDTIF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1997) to Swiss-Prot.
                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                           Hilschmann N.
                                                                                              POR2 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                       RESULT 13
POR2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porin,
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=AB; TISSUB=Whole, and Whole body;

MIDINE=2238825; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strain B.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,

A Hopkins R.F., Jozdan H., Moore T., Max S. I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toehiyvki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.M., Glay L.J., Hulyk S.M.,

Roaks S.A., McEwan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Nilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Rabeshey W., Helton E., Ketteman M., Madan A., Robrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeshey R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC042329; AAH42329.1;
EMBL; BC062525; AAH62525.1;
EMBL; BC062525; AAH62525.1;
EMBL; BC062526; AAH62525.1;
EMBL; BC065741; Embline Interpression of the companient of
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Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zon L.I.,
Kanki J.P., Look A.T., Chen Z.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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283 AA; 30284 MW; 935494C3B48DFB41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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g

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SEQUENCE FROM N.A.
STRAIN=breed White Leghorn; TISSUE=Lens fiber;
STRAIN=breed White Leghorn; TISSUE=Lens fiber;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF268470; AAF73513.1; ...
GO; GO:0005308; Fivoltage-dependent ion-selective channel act. ..; IEA.
GO; GO:0006820; P:anion transport; IEA.
InterPro; IPR001925; Porin_Euk.
InterPro; IPR001925; Porin_Euk.
PRATS; PR00185; EUKÄRYTORIN; 1.
PROSITE; PR00185; EUKÄRYTORIN; 1.
SEQUENCE 283 AA; 30198 MW; 4DB5DC020A632902 CRC64;
Voltage-dependent anion channel.
Name=VDAC2;
Gallus Gallus (Chicken).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TAXID=9031;
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2 KWDTDNTLGTEISWENKLAEGLKLTLDTIF 31 ò

Query Match
52.0%; Score 115; DB 2; Length 283;
Best Local Similarity 70.0%; Pred. No. 7e-07;
Matches 21; Conservative 6; Mismatches 3; Indels

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0; Gaps

Search completed: November 10, 2004, 12:27:05 Job time : 44.7654 secs

8175, Ap 61, Ap 61, Ap 4921, Ap 3.56, Ap 3. Appl 25, Appl 75, Appl 75, Appl 3746, Ap 397, App

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4822, Ap Sequence 1, Appli

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US-09-328-352-6261

US-09-809-665A-61

US-09-140-0114-011

US-09-140-014921

US-09-361-243-3

US-08-65-259-25

US-08-65-259-25

US-08-762-500-75

US-08-762-500-75

US-09-107-532A-3746

US-09-107-532A-3746

US-09-107-532A-3746

US-08-902-807-395

US-08-902-813-3

US-08-902-513-3

US-08-902-513-3
  US-09-328-352-8175
                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42535
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Best Local Similarity 56.77
Matches 17; Conservative
 US-09-270-767-57836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 57836, A Sequence 42535, A Sequence 24047, A Sequence 24047, A Sequence 46, Appl Sequence 758, Appl Sequence 17, Appl Sequence 15060, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20578, A Sequence 15487, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19310, A
Sequence 33, Appl
Sequence 27, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27, Appl
50, Appl
4, Appli
                                                                 November 10, 2004, 11:41:17; Search time 9.23302 Seconds (without alignments) 222.664 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence S
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                                                                                                                                                                                                                                                                                                       1: /cgn2_6/ptodata/l/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/l/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/l/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/l/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/l/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/l/iaa/PCTUS_COMB.pep:*
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-270-767-57836
US-08-451-715A-42535
US-08-270-767-42535
US-09-248-796A-24047
US-09-248-796A-24047
US-09-543-661A-7558
US-09-543-661A-7558
US-09-117-257-38
US-09-117-257-38
US-09-117-257-38
US-09-117-257-38
US-09-117-257-38
US-09-117-257-38
US-09-489-352-34
US-09-248-796A-1560
US-09-248-796A-1593
US-09-248-796A-1593
US-09-248-796A-1593
US-09-248-796A-1593
US-09-861-451A-50
US-09-861-451A-50
US-09-861-451A-50
US-09-861-451A-50
US-09-861-451A-50
US-09-861-451A-50
US-08-259-871A-1313-33
                                                                                                                       156
1 RGAVFSQDKDVVQBATKVLRNAADNFYINDR 31
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JS-09-032-438C-119
JS-09-874-923-120
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               protein search, using sw model
                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                            US-10-092-750-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                      Scoring table:
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                                             OM protein
                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                  Sequence:
                                                                                                                                                                                      Searched:
                                                                    Run on:
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No.
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Sequence 57836, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TOWNER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57836
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-00-270-767-42535

Sequence 42535, Application US/09270767

Sequence 42535, Application US/09270767

Sequence 42535, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

TILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 42235

LENGTH: 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
53.8%; Score 84; DB 4; Le
Best Local Similarity 56.7%; Pred. No. 2.5e-05;
Matches 17; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GAVFSODKDVVQEATKVLRNAADNFYINDR 31
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Guo, Betty
ITILE OF INVENTION: DDAA AND DDAB COMPOSITIONS AND METHODS OF USE
TILE REFERENCE: 4210.000500
CURRENT APPLICATION WUMBER: US/09/489,352
CURRENT APPLICATION WUMBER: DCT/US96/17081
EARLIER APPLICATION WUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-10-22
EARLIER APPLICATION WUMBER: 08/589,711
EARLIER APPLICATION WUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-24
NUMBER OF SEQ ID NOS: 66
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/09117257

Sequence 46, Application US/09117257

Patent No. 6214355

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Hook, Magnus

APPLICANT: Hanson, Mark

TITLE GO, Betty

APPLICANT: Hanson, Mark

TITLE REPERENCE: 4210.000500

CURRENT APPLICATION NUMBER: US/09/117,257

CURRENT FILING DATE: 1998-07-22

EARLIER APPLICATION NUMBER: OS/58/17081

ERALIER PILING DATE: 1996-01-22

EARLIER PILING DATE: 1996-01-24

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 46
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                                                                                                                                           DB 4; Length 191;
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Best Local Similarity 47.1%; Pred. No. 6.5;
Matches 8; Conservative 5; Mismatches
                                                                                                                                             Query Match
33.3%; Score 52; DB 4
Best Local Similarity 34.6%; Pred. No. 3.1;
Matches 9; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                   161 IFSDDEEVEEEAAPRIMDEFDGFYLH 186
                                                                                                                                                                                                                                                    4 VFSQDKDVVQEATKVLRNAADNFYIN 29
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US-03-489-352-46
; Sequence 46, Application US/09489352
; Patent No. 6312907
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43 KDIIDEINKIKKDAADN 59
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US-09-117-257-46
                         ; LENGTH: 191
, TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24047
SEQ ID NO 24047
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-117-257-46
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18-246-796A-24047

18-29-246-796A-24047

18-20-246-796A-24047

18-20-246-796A-24047

18-20-246-796A-24047

18-20-246-796A-24047

18-20-24-796A-24047

18-20-24-796A-24047

18-20-24-796A-24047

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18-20-24-796A-24047

18-20-24-796A-24047

18-20-24-796A-24047

18-20-24-796A-2608-13

18-20-24-796A-2608-13
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                                                                                                                                        Sequence 8, Application US/08451715A
Sequence 8, Application US/08451715A
Patent No. 5801013
GENERAL INFORMATION:
APPLICANT: Tou, Yan
APPLICANT: Houman, Fariba
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Helicobacter Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Strains Comprising Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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34.0%; Score 53; DB 1; Length 872;

Best Local Similarity 50.0%; Pred. No. 14;

Matches 11; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,715A FILING DATE: 26-MAY-1995 CLASSIPICATION: 435
     508 GAVFGQDEDFVKCALQEFKMAAGNFYINDK 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERNICE/DOCKET NUMBER: CP194-25
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      617 KSRLNSATKEARNALDNYRFND 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING.SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 KDVVQEATKVLRNAADNFYIND 30
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MEDIUM TYPE: Floppy
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Hook, Magnus
APPLICANT: Hook, Magnus
APPLICANT: Hanson, Mark

TITLE OF INVENTION: DbpA AND DbpB COMPOSITIONS AND METHODS OF USE
FILE REPERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/489,352
CURRENT PILING DATE: 1000-01-21
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Parentin Ver. 2.1
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ## Sequence 17, Application US/09117257
## APPLICANT: Hook, Magnus
## TITLE OF INVENTION: DopA AND DopB COMPOSITIONS AND METHODS OF USE
## TITLE REFERENCE: 4210.000500
## CURRENT FILING DAID: 1998-07-22
## BARLIER FILING DAID: 1996-10-22
## BARLIER FILING DAID: 1995-01-22
## BARLIER FILING DAID: 1995-04-24
## NUMBER OF SEQ ID NOS: 66
## SOFTWARE: PatentIN Ver. 2.1
## SEQ ID NO 17
## IENGTH: 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 194;
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                                                                                               US-09-489-352-38
Sequence 38, Application US/09489352
, Patent No. 6312907
            43 KDITDEINKIKKDAADN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Borrelia burgdorferi
US-09-489-352-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 KDVVQEATKVLRNAADN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 KDITDEINKIKKDAADN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Borrelia burgdorferi
US-09-117-257-17
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Best Local Similarity
Matches 8, Conserve
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US-09-117-257-17
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5558
LENGTH: 340
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Patent No. 6214355

GENERAL INFORMATION

APPLICANT: Hook, Magnus

APPLICANT: Guo, Betty

APPLICANT: Guo, Betty

APPLICANT: Guo, Betty

APPLICANT: Guo, Betty

CURRELL APPLICATION UNDER: US/09/117, 257

CURRENT APPLICATION NUMBER: DS/09/117, 257

CURRELTE FILING DATE: 1996-07-22

EARLIER PILING DATE: 1996-10-22

EARLIER PILING DATE: 1996-10-22

EARLIER PILING DATE: 1996-01-22

EARLIER FILING DATE: 1996-01-22

EARLIER FILING DATE: 1996-01-24

NUMBER OF SEQ ID NOS: 66

SEQ ID NOS: 66

SEQ ID NOS: 84

LENGTH: 160
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Pred. No. 26;
7; Mismatches 13; Indels
                                                                         DB 3; Length 195;
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                                                                                                                     4; Indels
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                                                               Query Match
32.1%; Score 50; DB
Best Local Similarity 47.1%; Pred. No. 6.5,
Matches 8; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                  US-09-543-681A-7558
; Sequence 7558, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                             9 KDVVQEATKVLRNAADN 25
                                                                                                                                                                                          43 KDIIDEINKIKKDAADN 59
9 KDVVQEATKVLRNAADN 25
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Best Local Similarity 33.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-681A-7558
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US-09-489-352-34
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| FALENT NO. 93 1230.
| APPLICANT: Hook, Magnus
| APPLICANT: Hook, Magnus
| APPLICANT: Hanson, Mark
| TITLE OF INVENTION: DbpA AND DbpB COMPOSITIONS AND METHODS OF USE
| PILE REFERENCE: 4210.000500
| CURRENT APPLICATION NUMBER: US/09/489,352
| CURRENT FILING DATE: 2000-01-21
| EARLIER FILING DATE: 1996-10-22
| FARLIER FILING DATE: 1996-01-22
| EARLIER FILING DATE: 1996-01-22
| EARLIER FILING DATE: 1996-01-22
| EARLIER FILING DATE: 1996-01-22
| BARLIER FILING DATE: 1996-01-22
| SOFTWARE: PROPERTION NUMBER: 08/427,023
| BARLIER FILING DATE: 1996-04-24
| SOFTWARE: PALENT NUMBER: 1996-04-24
| SOFTWARE: PALENT NUMBER: 1906-04-24
| SOFTWARE: PALENT NUMBER: 1906-04-24
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                                                                                                                                                                   DECORIN BINDING PROTEIN COMPOSITIONS AND METHODS OF USE
US-08-945-476-17

US-08-945-476-17

Sequent No. 6248517

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: DECORIN BINDING PROTEIN COMPOSITIONS

TITLE OF INVENTION: METHODS OF USE

TITLE OF SEQUENCES: 2

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/08/945,476

FILING DATE:

PRILOR DATE:

PRILOR DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
30.1%; Score 47; DB 3; Length 194;
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/589,711
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,023
FILING DATE: 24-APR-1995
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09489352
Patent No. 6312907
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US-09-489-352-17
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amino acid
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Sequence 34, Application US/09489352

Patent No. 61207

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Hook, Magnus

APPLICANT: Honson, Mark

ITLE OF INVENTION: DDPA AND DDPB COMPOSITIONS AND METHODS OF USE

TILE REFERENCE 4210.000500

CURRENT APPLICATION NUMBER: US/09/489,352

CURRENT FILING DATE: 2000-01-21

EARLIER APPLICATION NUMBER: 08/589,711

EARLIER PLILNG DATE: 1996-01-22

EARLIER FILING DATE: 1996-01-22

EARLIER FILING DATE: 1996-01-24

EARLIER FILING DATE: 1996-01-24

EARLIER FILING DATE: 1996-01-24

SARLIER PLILNG DATE: 1996-01-24

SARLIER PLING DATE: 1995-04-24

SOMPTANDED: DELGATION NUMBER: OS/427,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                             APPLICANT: Hook, Magnus
APPLICANT: Guo, Betry
APPLICANT: Hanson, Mark
APPLICANT: Hanson, Mark
TITLE OF INVENTION: Dbpa AND Dbpa COMPOSITIONS AND METHODS OF USE
FILE REPRENENT: 420-000650
CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT PILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER PILING DATE: 1996-10-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-24
SALIER PILING DATE: 1996-01-24
SALIER PILING DATE: 1996-01-24
SALIER PILING DATE: 1996-01-24
SALIER PILING DATE: 1996-01-34
SEQID NO 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.1%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 5; Indels
Sequence 34, Application US/09117257
Patent No. 6214355
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KDVVQEATKVLRNAADN 25
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; ORGANISM: Borrelia burgdorferi
US-09-489-352-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 KDITDEINKIKKDAADN 59
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US-09-117-257-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 KDVVQEATKVLRNAADN 25
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RESULT 15

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US-09-248-796A-15060

Sequence 15060, Application US/09248796A

Pacent No. 6747137

CENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PLING DATE: 1998-08-13

PRIOR PLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15660

LENGTH: 398

TYPE: PRI

CORGANISM: Candida albicans

US-09-248-796A-15060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 10, 2004, 12:32:27 Job time: 10.233 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

1007 61.10. TT 77.11 AON 111

OM protein - protein search, using sw model

November 10, 2004, 15:53:52; Search time 29.8997 Seconds (without alignments) 366.225 Million cell updates/sec Run on:

US-10-092-750-13 156 1 RGAVPSQDKDVVQEATKVLRNAADNFYINDR 31

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1566620 seqs, 353225886 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/PCT_NEW PUBLOBD:*

2: /cgn2_6/prodata/1/pubpaa/PCT_NEW PUBLOBD:*

3: /cgn2_6/prodata/1/pubpaa/USO6_NEW PUBL.pep:*

4: /cgn2_6/prodata/1/pubpaa/USO6_NEW PUBL.pep:*

5: /cgn2_6/prodata/1/pubpaa/USO7_NEW PUBL.pep:*

6: /cgn2_6/prodata/1/pubpaa/USO8_NEW PUBL.pep:*

7: /cgn2_6/prodata/1/pubpaa/USO8_NEW PUBL.pep:*

8: /cgn2_6/prodata/1/pubpaa/USO8_NEW PUBL.pep:*

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10: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*

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14: /cgn2_6/prodata/1/pubpaa/USO9_NEW PUBL.pep:*

15: /cgn2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubpaa/USIOP_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/USIOD_PUBCOMB.pep:*

19: /cgn2_6/prodata/1/pubpaa/USIOD_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpaa/USIOD_PUBCOMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

 	13, Appl	384, App	•	2507, Ap	22859, A	13433, A	19524, A	3745, Ap	8341, Ap	18, Appl	22032, A	10453, A	10260, A
Description	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	Sequence
ΩΙ	US-10-092-750-13	US-10-043-487-384	US-10-408-765A-1800	US-10-369-493-2507	US-10-369-493-22859	US-10-369-493-13433	US-10-369-493-19524	US-10-369-493-3745	US-10-369-493-8341	US-10-230-331-18	US-10-369-493-22032	US-10-369-493-10453	US-10-156-761-10260
DB	14.	14	16	14	14	14	14	14	14	14	14	14	14
% Query Match Length	31	308	563	548			544	552	402	211	575	542	543
% Query Match	100.0	90.4	90.4	61.5	57.7	57.1	56.4	51.3	50.0	49.4	49.4	48.7	42.9
Score	156	141	141	96	06	80	88	80	78	77	77	76	67
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ALIGNMENTS

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Gaps
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  | Sequence 13, Application US/10092750
| Sequence 13, Application US/10092750
| Publication No. US2003003157A1
| GENERAL INFORMATION:
| APPLICANT: Hammond, Philip W.
| APPLICANT: Alpin, Julia APPLICANT: Alpin, Julia APPLICANT: Wright, Martin C.
| TITLE OF INVENTION: POLYPEPTIGES INteractive with BCL-X1
| FILE REFERENCE: 50036/050002
| CURRENT APPLICATION NUMBER: US/10/092,750
| PRIOR PLILING DATE: 2001-03-09
| PRIOR FILING DATE: 2001-03-08
| NUMBER OF SEQ ID NOS: 253
| SEQ ID NO 13
| LENGTH: 31
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100.0%; Score 156; DB 14
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 31; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-13
US-10-092-750-13
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1 RGAVFSODKDVVQEATKVLRNAADNFYINDR 31 1 RGAVFSQDKDVVQEATKVLRNAADNFYINDR 31 셤 ઠે

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RESULT 2
US-10-043-487-384
is Sequence 384, Application US/10043487
is Publication No. US20030055220A1
igeneral information:

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APPLICANT: Cao, Yongwel
APPLICANT: Cao, Yongwel
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT PAPPLICATION NUMBER: US, 10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US, 60/360, 039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22859
LENGTH: 553
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APPLICANT: Cao, Yongwei
APPLICANT: AIRALe, Gregory J.
APPLICANT: Stater, Stewen C.
APPLICANT: Stater, Stewen C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERINS
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERINS
FILE REFERENCE: 38-10(5205.2)
FILE REFERENCE: 38-10(5205.2)
FILE REFERENCE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
FILENCE OF SEQ ID NOS: 47374
SEQ ID NO 13433
LENGTH: 622
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Best Local Similarity 53.3%; Pred. No. 0.00018;
Matches 16; Conservative 8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 GSVFAKDREAILKAEKALRYAAGNFYINDK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
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        CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22859, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13433, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              TYPE: PRT; CRGANISM: Schizosaccharomyces pombe
US-10-369-493-2507
                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-10-369-493-22859
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US-10-369-493-13433
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APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
FILE REFERENCE: B4778A
CURRENT APPLICATION WUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEO ID NOS: 561
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2507, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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GENERAL SEQUENT:
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Sequence 1800, Application US/10408765A;
PUBLICARI NO. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEMNIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION UMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1800
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90.4%; Score 141; DB 14; Length 308;
Best Local Similarity 93.3%; Pred. No. 2.7e-12;
Matches 28; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 GAVFSQDKDVVQEATKVLRNAAGNFYINDK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 GAVFSÓDKDVVOBATKVLRNAAGNFYINDK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3%
...hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-408-765A-1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-369-493-2507
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 384
LENGTH: 308
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FIL NOV LZ L4:54:49 ZU04

FEATURE:
NAME/KSY: unsure
LOCATION: (1)..(622)
COCHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13433

TYPE: PRT ORGANISM: Aspergillus nidulans

2 GAVFSQDKDVVQEATKVLRNAADNFYIN 29

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Sequence 8341, Application US/10369493

Publication No. US20030233675A1

Sequence 8341, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT APPLICATION NUMBER: US/10/369, 493

FRIGR APPLICATION NUMBER: US 60/360, 039

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 8341

LENGHH: 402
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                                                                                                                                                                                              Gaps
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Pred. No. 0.0071;
6; Mismatches 9; Indels
                                                                                                                                     Length 552;
                                                                                                                                                                                              6; Indels
                                                                                                                                  Query Match
Best Local Similarity 50.0%; Pred. No. 0.0053;
Matches 14; Conservative 8; Mismatches 6
; NAME/KEY: unsure
; LCCATION: (1)..(552)
; CTBE INFORMATION: unsure at all Xaa locations
US-10-369-493-3745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 GAIIATDRAAILAATRQLRFAAGNFYINDK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                                                                    470 GSIFASDRSVIRFAEEKLRNSAGNFYIN 497
                                                                                                                                                                                                                                                2 GAVFSQDKDVVQEATKVLRNAADNFYIN 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-369-493-8341
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Sequence 19224, Application US/10369493

Sequence 19224, Application No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Goo' Yongwei

APPLICANT: Glodman, Barry S.

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (5205.) B.

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

EENTH: 544
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                                                                                                                                                                                                               Query Match
57.1%; Score 89; DB 14; Length 622;
Best Local Similarity 60.7%; Pred. No. 0.00029;
Matches 17; Conservative 5; Mismatches 6; Indels
```

ö Gaps FEATURE: ; OTHER INFORMATION: Diacylglycerol Acyltransferase Protein Sequence US-10-230-331-18 49.4%; Score 77; DB 14; Length 211; 46.7%; Pred. No. 0.0045; tive 7; Mismatches 9; Indels TYPE: PRT ORGANISM: Artificial Sequence Query Match
Best Local Similarity 46.7
Matches 14; Conservative

Sequence 3745, Application US/10369493

Sequence 3745, Application US/10369493

Publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gldman, Barry S.

PRIOR REPERENCE: 38-10 (5202)B

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 3745

LENGTH: 552

TYPE: PRT ORGANISM: Neurospora crassa FEATURE:

RESULT 8 US-10-369-493-3745

; TYPE: PRT ; ORGANISM: Myxococcus xanthus US-10-369-493-19524

Fri Nov 12 14:54:49 2004

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335 RVTVFRQEDEVTRTATLVLRGATQN-HLDD 363

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Sequence 343, Application US/10369493

Sequence 343, Application WS/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

TILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B.

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,039

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 3433

LENGTH: 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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34.3%; Score 53.5; DB 14;
Best Local Similarity 43.3%; Pred. No. 40;
Matches 13; Conservative 6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(537)
; OTHER INFORMATION: unsure at all.Xaa locations US-10-369-493-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
42.9%; Score 67; DB 14
Best Local Similarity 50.0%; Pred. No. 0.42;
Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 GAVVSNDRAAAYTMDKLRYAAGNFYINDK 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGAVFSQDKDVVQEATKVLRNAADNFYIND 30
                                                                                                                                                                                                      APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRAWA, HINCHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERRNCE: 249-226
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GAVESODKDVVQEATKVLRNAADNFYINDR 31
                                                                                                    Sequence 10260, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces avermitilis US-10-156-761-10260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Neurospora crassa
                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure LOCATION: (1)..(9
                                              RESULT 13
US-10-156-761-10260
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US-10-369-493-3433
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                                                                                                                                                                 Sequence 2203.2 Application US/10369493

Publication No. US2030233675A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gardy Yongwei
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Goddman, Barry S.
APPLICANT: Glater, Marfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10 (52052)B
CURRENT FILING DATE: 2003-02-28
FRICK APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22032
LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Alace, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10453
LENGTH: 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 49.4%; Score 77; DB 14; Length 575; Best Local Similarity 43.3%; Pred. No. 0.015; Matches 13; Conservative 10; Mismatches 7; Indels
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: LOCATION: (1)..(542)

: CTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-10463
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GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GAVESODKDVVQEATKVLRNAADNFYINDR 31
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; Sequence 10453, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cytophaga hutchinsonii
                                                                                                                                       RESULT 11
US-10-369-493-22032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-369-493-22032
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US-10-242-1247-257,

Publication No. US20040029122A

Publication No. US2004002912A

APPLICANT: Wang, Liangeu

FILE REPRENCE: ELITRE 003-02-20

CURRENT FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PEPLICANTION NUMBER: 60/230, 347

PRIOR APPLICANTION NUMBER: 60/230, 385

PRIOR APP
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; ORGANISM: Clostridium botulinum
US-10-282-122A-52577
```

ô Gaps ö Query Match
Best Local Similarity 40.0%; Pred. No. 18; Length 241;
Matches 10; Conservative 6; Mismatches 9; Indels 4 VFSODKDVVQEATKVLRNAADNFYI 28 à

70 VFSDDLETMEKEAEVLGNLGENVYI 94 g Search completed: November 10, 2004, 16:35:49 Job time : 30.8997 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 6.26698 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-13 156 1 RGAVFSQDKDVVQEATKVLRNAADNFYINDR 31 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

P72673

probable delta-1-pyrrolline-5-carboxylate dehydrogenase APE0807 - Aeropyrum pernix (strair probable delta-1-pyrrolline-5-carboxylate dehydrogenase APE0807 - Aeropyrum pernix (strair C,Species: Aeropyrum pernix
C,Species: Aeropyrum pernix
C,Saccession: A72673

R,Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999

A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyri

RESULT 2

hypothetical prote	probable thiamine-	hypothetical prote	hypothetical prote	valine-tRNA ligase	retrovirus-related	retrovirus-related	disease resistance	disease resistance	ribosomal protein	con-8 protein - Ne	mutator mutT (AT-G	30S ribosomal prot	DNA polymerase i (phenylalanine-tRNA	glutamine syntheta
F96634	A64152	865227	B84647	E71852	S64734	526840	T51140	T51141	863968	802210	164101	AC0128	H90601	AE0296	H83944
7	~	~	N	7	(7	(7	~	N	Н	~	~	N	N	N	N
191	226	583	693	872	1009	1009	1217	1217	62	176	234	241	297	327	449
31.1	30.8	30.8	30.8	30.8	30.8	30.8	30.4	30.4	30.1	30.1	30.1	30.1	30.1	30.1	30.1
48.5	48	48	48	48	48	48	47.5	47.5	47	47	47	47	47	47	47
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Rill, X.; Kounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h. X.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.c. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1998
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:050443; GB:AL010186; GB:AL123456; NID:g3261493; PIDN:CAA15864; A;Experimental source: strain H37RV C;Genetics: C;Genetics: A;Genetics: C;Cycle: rock C;Cycle: c;Cycl
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: C70877 A;Accession: C70877 A;Status: precliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-543 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Note: SCIC2.01
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g22810 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84617
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A;Cross-references: UNIPROT:Q8CJR1; EMBL:AL031124; PIDN:CAA19968.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%; Score 72; DB 2; Length 543; 50.0%; Pred. No. 0.031; vative 4; Mismatches 11; Indels
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C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
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325 GSVISNDRAAAYTMEKLRYAAGNFYINDK 354
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Best Local Similarity 46.73
Matches 14; Conservative
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Best Local Similarity
Local 15; Conserva
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;Molecule type: DNA
;Molecule type: DNA
;Cross-references: UNIPROT:P07275; EMBL:U00062; NID:g488162; PIDN:AAB68907.1; PID:g4881
;Krzywicki, K.A.; Brandriss, M.C.
ol. Cell. Biol. 4, 2837-2842, 1984
;Title: Primary structure of the nuclear PUT2 gene involved in the mitochondrial pathwa
;Reference number: S05876; MUID:85137477; PMID:6098824
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                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9YDW2; DDBJ;AP000060; NID:g5104188; PIDN:BAA79785.1; PID:g5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) precursor - yeast (Saccharomyces Alternate names: protein H8179.11; protein YHR037w Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Stajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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C:Date: 31-Mar-1991 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: S46738; S05876
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;Cross-references: EMBL:M10029; NID:g172302; PIDN:AAA34924.1; PID:g172303
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F;101-371/Domain: aldehyde dehydrogenase homology <ALDD>
F;317,351/Active site: Glu, Cys #status predicted
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49.4%; Score 77; DB 1; Length 575
Best Local Similarity 43.3%; Pred. No. 0.0064;
Matches 13; Conservative 10; Mismatches 7; Indels
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A;Description: The sequence of S. cerevisiae cosmid 8179.
A;Reference number: $46732
        A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A72673
A;Status: preliminary
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GSVFAKDREAILKAEKALRYAAGNFYINDK 497
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A;Cross-references: SGD:S0001079; MIPS:YHR037w
A;Map position: 8R
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Best Local Similarity
Thes 16; Conserva
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A, Gene: APE0807
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58.8%;

Best Local Similarity 58.8 Matches 10; Conservative

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C;Species: Helicobacter pylori
C;Date: 09-Jug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Date: 09-Jug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64664
B;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A,Authors: Wallin, E.; Hayes, W.S.; Borcdovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.
A,Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A,Reference number: A64520; MulD:97394467; PMID:9252185
A,Accession: A64664
A,Fatus: preliminary, nucleic acid sequence not shown; translation not shown
A,Rolecule type: DNA
A,Ross-references: UNIPROT:P56000; GB:AE000621; GB:AE000511; NID:92314301; PIDN:AAD08199: C; Keywords: ligase
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H82492
conserved hypothetical protein VGA0167 [imported] - Vibrio cholerae (strain N16961 serogy)
CJSpecies: Vibrio cholerae
CJSCSSION: H82492
R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
CJACGSSION: H82492
A,THIA: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A,Reference number: A82035; MUID:20406833; PMID:10952301
A,Retauts: preliminary
A,Nolecule type: DNA
A,Residues: 1-262 <HEI>
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A;Map position: 1.4/2: 227/2; 337/3; 544/2; 626/3; 661/1; 776/1; 964/3; 1153/2; 1720/2; 1875/3;
A;Introns: 14/2: 227/2; 37/3; 544/2; 626/3; 661/1; 776/1; 964/3; 1153/2; 1720/2; 1875/3;
C;Superfamily: DNA-directed DNA polymerase II
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2.712
R;Cottage, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19463
A;Reference number: Z19463
A;Reference number: C10712
A;Reference number: C107
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; Pred. No. 27;
2; Mismatches
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34.0%; Score 53; DB
Best Local Similarity 41.7%; Pred. No. 74;
Matches 10; Conservative 6; Mismatches
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54 QPSELVDEQTKVIISVVDYFFISD 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KDVVQEATKVLRNAADNFYIND 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.0%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
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GNAUGH
M polyprotein precursor - bunyamwera virus
N Contains: glycoprotein G1; glycoprotein G2; nonstructural protein
C,Species: bunyamwera virus
R,Lees, J.F.; Pringle, C.R.; Elliott, R.M.
Wirology 148; 1-14; 1986
A,Title: Nucleotide sequence of the Bunyamwera virus M RNA segment: conservation of stru
Virology 148; 1-14; 1986
A,Title: Nucleotide sequence of the Bunyamwera virus M RNA segment: conservation of stru
A,Reference number: A04101; MUID:86098655; PMID:3753629
A,Ference number: A04101; MUID:86098655; PMID:3753629
A,Residues: 1-1433 - LEE>
A,Forolecule type: genomic RNA
A,Residues: 1-1433 - LEE>
A,Forolecule type: genomic cleavages in vivo yield mature proteins including nonstruc
C,Genmentics:
A,Map position: segment M
C;Superfamily: bunyavirus M polyprotein;
C,Feywords: glycoprotein; nonstructural protein; polyprotein; transmembrane protein
C,Feywords: glycoprotein sequence #status predicted <AMPP>
F,1-16/Domain: signal sequence #status predicted <AMPP>
F,1-16/Domain: signal sequence #status predicted <AMPP>
F,1-16/Domain: signal sequence (ASP)
F,1-1433/Product: M polyprotein #status predicted <AMPP>
F,1-1433/Product: M polyprotein #status predicted <AMPP>
F,60,248,624,1169/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                         Gaps
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A64664
valine-tRNA ligase (EC 6.1.1.9) - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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35.9%; Score 56; DB 1; Length 1433;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 12; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 804;
                                                         Indels
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                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.2%; Score 58; DB 2; Best Local Similarity 55.0%; Pred. No. 4.7; Matches 11; Conservative 6; Mismatches
             Fred. No. 2.6;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071 GCVFGSCQDVIRPETKVYRKAVDEVVI 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: strain S288C
C, Genetics:
A, Gene: SGD: SCYI
A, Cross-references: SGD: S0003051; MIPS: YGL083w
A, Map position: 7L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GAVESODKDVVQEATKVLRNAADNFYI 28
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|:|| ::||| ::||| |:| 71 SRDKVLIQEAYEILRNQANN 90 SODKDVVQEATKVLRNAADN 25

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Clacesion: T4028
Ribne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Submitted to the EMBL Data Library, October 1998
A.Reference number: Z21868
A.Reference number: Z21868
A.Reference number: T40258
A.Reference number: T40258
A.Relatus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-546 <LYN>
A.Residues: 1-546 <LYN>
A.Residues: Loure: Strain 972h-; cosmid G337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable t-complex protein 1, theta subunit - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                       SENI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 1976.1; protein YLR430w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53416; A44387; §41985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 'MHS',130,'FCEREVQ',131-2231 <DEM>
A;Cross-references: GB:M74589; NID:g172573; PIDN:AAB63976.1; PID:g172574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
32.7%; Score 51; DB 2; Length 223
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Description: may be component of nuclear splicing complex C, Keywords: nucleotide binding; nucleus; P-loop F,1357-1364/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                            R)Favello, A. submitted to the EMBL Data Library, February 1995 A;Description: The sequence of S. cerevisiae cosmid 9576. A;Reference number: 553409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.4%; Score 50.5; DB 2; Best Local Similarity 43.3%; Pred. No. 36; Matches 13; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SPDB:SPBC337.05c
A;Map position: 4
A;Introns: 41/3; 55/1; 95/3
C;Superfamily: molecular chaperone t-complex-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 RVTVFROVEDITRIATIVLRGATKT-YLDD 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGAVFSQDKDVVQEATKVLRNAADNFYIND 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: SGD:S0004422; MIPS:YLR430w
A;Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673 IFSSDKHLYQAATNILYNTFD 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VFSQDKDVVQEATKVLRNAAD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SGD: SEN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figlacer, P., Francell, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 252. 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUD:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-713 <GLAA
A;Cross-references: UNIPROT:Q928G9; GB:AL592022; PIDN:CAC97793.1; PID:g16415088; GSPDB:G
A;Experimental source: strain Clip11262
A,Cross-references: UNIPROT:Q9KMZ9; GB:AE004357; GB:AE003853; NID:g9657547; PIDN:AAF9606
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
Modecule type: DNA
A;Residues: 1-1153 «ADA»
A;Cross-references: UNIPROT:P50493; EMBL:M90694; NID:g160290; PID:g160291; PIDN:AAA29603
                                                                                                                                                                                                                                                                                                                                                                                                                                                           endopeptidase [bacteriophage bIL285] homolog lin2566 [imported] - Listeria innocua (stra
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28652
R;Adams, J.H.; Sim, B.K.; Dolan, S.A.; Fang, X.; Kaslow, D.C.; Miller, L.H. Proc. Natl. Acad. Sci. U.S.A. 89, 7085-7089, 1992
A;Title: A family of erythrocyte binding proteins of malaria parasites.
A;Reference number: Z20495; MuID:92357776; PMID:1496004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI1752
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                 Length 262;
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Pred. No. 71;
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 2; Length 713;
Pred. No. 30;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                    -----KDVVQEATKVLRNAADNF 26
                                                                                                                                                                 5
                                                                                                                                                               Score 52.5; DB Pred. No. 8.1; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erythrocyte binding protein - Plasmodium knowlesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 FSQDKDVVQEATKVLRNAADNFY 27
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                                                                                                                                                            Query Match
Best Local Similarity 30.2%;
Matches 13; Conservative 5
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ilarity 47.8%;
Conservative
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Best Local Similarity 42.9%;
Matches 9; Conservative
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A,Introns: 20/3; 1087/3; 1114/2
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Best Local Similarity
Matches 11; Conserv
                                                                                                           A; Map position: 2
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A;Gene: lin2566
                                                                                  A;Gene: VCA0167
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                                                     C; Genetics:
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Matches
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RESULT 13

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Search completed: November 10, 2004, 12:29:16 Job time : 7.26698 secs

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PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                                                     P30038 homo sapien
081238 homo sapien
070p27 rattus norv
08r0n1 mus musculu
08r1s2 mus musculu
08bxn3 mus musculu
08bxn3 mus musculu
079y23 brachydanio
079y24 certopyrum p
01648 caenorhabdi
09h310 emericella
09h310 emericella
09hxr5 leishmania
09hxr5 leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Offw05 candida gla

09vnx4 drosophila

08130 drosophila

07mv36 porphyromon

05bh88 debaryomyce

07sd4 neurospora

07275 saccharomyc

07288 kluyveromyc

07043 mycobacteri

070068 mycobacteri

070089 anopheles g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q75ez9 ashbya goss
Aas50295 ashbya go
Q6cf74 yarrowia li
Q7vsi8 bordetella
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                                                                     November 10, 2004, 11:27:01; Search time 33.9182 Seconds (without alignments) 525.871 Million cell updates/sec
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Aas04910
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                          US-10-092-750-13
156
1 RGAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                          lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUT2_HUMAN
Q961238
Q961238
Q961270
Q77P27
Q8878011
Q8878011
Q887802
Q787702
Q7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length
                                                 protein search,
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                            Database
                                                                         Run on:
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Result

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Q82jn1 streptomyce
Q82jr1 streptomyce
P7568 drosophila
Q95cy8 drosophila
Q8in17 drosophila
Q8in18 drosophila
Q81D4 hordeum vul
Q81D6 hordeum vul
Q81D6 bacillus th
Q6hnq7 bacillus ce
Q81yg7 bacillus an
A839550 bacillus an
A839550 bacillus an
0827N1
098CJR1
PUT2 AGABI
095TY
095TY
081N17
091N18
081N18
081LB4
081LB4
061LB4
061LB4
073DU5
073DU5
073DU5
0AAN39550
 691111111111
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ALIGNMENTS

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VARIATY HPII LEU-352, AND VARIANT LEU-16.
MEDLINE=98367029; PubMed=9700195;
MEDLINE=98367029; PubMed=9700195;
MEDLINE=98367029; PubMed=9700195;
Geraghty M.T., Vaughn D., Nicholson A.J., Lin W.-W.,
Jimenez-Sanchez G.,
Obie C., Plynn M.P., Valle D., Hu C.-A.A.;
Mutations in the Deltal-pyrroline 5-carboxylate dehydrogenase gene
cause type II hyperprolinemia.";
Hum. Mol. Genet. 7:1411-1415(1998)
-!- FUNCTION: Irreversible conversion of delta-1-pyrroline-5-
-!- FUNCTION: Irreversible conversion of delta-1-pyrroline, to
glutamate. This is a necessary step in the pathway interconnecting
the urea and tricarboxylic acid cycles. The pathway interconnecting
the urea and tricarboxylic acid cycles. The preferred substrate is
glutamic gamma-semialdehyde, other substrates include succinic,
PUTZ HUMAN STANDARD; PRI; 563 AA.
P912 HUMAN STANDARD; PRI; 563 AA.
P913018; Q16882.
01-APR-1993 (Rel. 25, Created)
01-APR-1997 (Rel. 35, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
05-UTL-2004 (Rel. 44, Last annotation update)
Name-ALDH4A1; Synonyms-PSCDH, ALDH4;
HOMO sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelecstomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDISOBERGIADBY, and Retina,

MEDISOBERGIADBY, PubMede2621661;

Hu C.-A., Lin W.-W., Valle D.;

Hu C.-A., Lin W.-W., valle D.;

Gloning, characterization, and expression of cDNAs encoding human delta 1-pyrroline-5-carboxylate dehydrogenase.";

J. Biol. Chem. 271:9795-9600(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human liver glutamic gamma-semialdehyde dehydrogenase: structural relationship to the yeast enzyme.";
Comp. Blochem. Physiol. 102B:791-793(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 25-35.

TISSUB-Liver;

MEDLINE=93162045; PubMed=1286669;

HOCHSTRASSED D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,

Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas I.

Appel R.D., Hughes G.J.;

"Human liver protein map, a reference database established by microsequencing and gel comparison.";

Ejectrophoresis 13:992-1001(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
MEDLINE=93009642; PubMed=1395511;
Hempel J., Eckey R., Berie D., Romovacek H., Agarwal D.P.,
Goedde H.W.;
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TISSUB-LUNG;

ADDINE-25388257; PubMed=12477932;

ADDINE-25388257; PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhar N.K.,

A Alschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhar N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toschivyki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.R., Gunarate P.H.,

Richards S., Worley K.C., Hale S., Garcia A.R., Gubbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

A Jones S.J., Marra M.A.,

Rodersation and initial analysis of more than 15,000 full-length human
                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01.MAR-2003 (TrEMBLrel. 23, Created)
01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2004 (TrEMBLrel. 26, Last annotation update)
Aldehyde dehydrogenase 4A1,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl: Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                            Name=ALDH4A1;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                      pancreas.

DISEASE: Defects in ALDH4A1 are the cause of hyperprolinemia type DISEASE: Defects in ALDH4A1 are the cause of hyperprolinemiation of delta-1-pyrroline-5-causally related to neurologic manifestations, including seizures and mental retardation.

SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                          -!- SUBUNIT: Homodimer.
-!- SUBCELIAR LOCATION: Mitochondrial matrix.
-!- TISSUB SPECIFICITY: Highest expression is found in liver followed by skeletal muscle, kidney, heart, brain, placenta, lung and
glutaric and adipic semialdehydes. CATALYTIC ACTIVITY: 1-pyrroline-5-carboxylate + NAD(+) + \rm H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
By similarity.
P -> L (in allel ALDH4A1*4).
/FTIG=VAR 002259.
S -> L (in HPII; allele ALDH4A1*3).
/FTIG=VAR 002260.
P -> L (in Ref. 2).
D -> E (in Ref. 2).
W; 8B864771B7DB5FF8 CRC64;
                          L-glutamate + NADH.
-!- PATHWAY: Conversion from proline to glutamate; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.4%; Score 141; DB 1; Length 563; Best Local Similarity 93.3%; Pred. No. 9.4e-11; Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61751 MW;
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U24266; AAC50500.1; -. SWISS-2DPAGE; P30038; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                         OGP; P30038; -.
Genew; HGNC:406; ALDH4A1.
Reactome; P30038; -.
MIM; 606811; -.
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314
348
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563 AA;
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ACT SITE
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TISSUE=Lung;
Sutrauberg R.;
Sutrauberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023600, AAH23600.1;
EMBL; BC025509, Cimitcohondrial matrix; IEA.
GO; GO:0005759; Cimitcohondrial matrix; IEA.
GO; GO:0005759; F:-pyrrolline-5-carboxylate dehydrogenase act. . .; IEA.
GO; GO:0004912; F:-pretabolism; IEA.
GO; GO:0006151; P:metabolism; IEA.
GO; GO:0005651; P:prolline biosynthesis; IEA.
InterPro; IFR002086; Aldehyde dehydr.
InterPro; IFR002081; Dipyr5carbox1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%; Score 141; DB 2; Length 563; 93.3%; Pred. No. 9.4e-11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                      PEAM, PF00171; Aldedh, 1.
TICRFAMS, TICRO1216; Dipyr5carbox1; 1.
PROSITE; PS00070; ALDEHYDE DEHYDR CLU; UNKNOWN 1.
SEQUENCE; PS00687; ALDEHYDE GLU; UNKNOWN 1.
SEQUENCE 563 AA, 61719 WW, 4D964771B7DB5FPD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Aldehyde dehydrogenase 4A1,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 93.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=ALDH4A1;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Gaps

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563 AA

PRELIMINARY;

Q81Z38 Q81Z38;

RESULT 2 Q81Z38 ID Q8 AC Q8

GAVFSQDKDVVQEATKVLRNAAGNFYINDK 509 2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31

480

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Gaps

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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MILLARE=2388257; PubMed=12477932;
MILLARE=2388257; PubMed=12477932;
MILLARE R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninch P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
GO; GO:0003842; F:1-pyrroline-5-carboxylate dehydrogenase act. . .; IEA. GO; GO:0004541; F:oxidoreductase activity; IEA. GO; GO:000452; P:metabolism; IEA. GO; GO:0005561; P:metabolism; IEA. GO; GO:0005561; P:proline biosynthesis; IEA. InterPro; IPR0012086; Aldehyde dehydr. InterPro; IPR0012086; Aldehyde dehydr. InterPro; IPR0012086; Aldehyde dehydr. InterPro; IPR00131; DIDYScarbox1. Pfam; PF00111; Aldehyd. ANF receptor. ITGRFAMS; TIGR01235; DIDYScarbox1. Pfam; PF001094; ANF receptor. ITGRFAMS; TIGR01235; DIDYScarbox1. I. PROSITE; PS000677; ALDEHYDE GLHYDR GLY; UNKNOWN 1. SEQUENCE 1465 AA; 163958 MM; E50B012FFDEF84EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124, DB 2; Length 14
Pred, No. 5.7e-08;
5; Mismatches 2; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00171; Aldedh; î.
TIGRFAMs; TIGR01236; DIpyr5carbox1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=A930035F14R1k; Synonyms=Aldh4al;
Mus musculus (Mouse)
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HSSP, P05091, 1002.
MGD, MG1.2443831, A330035F14Rik.
InterPro, IPR002086, Aldehyde dehydr.
InterPro, IPR002086, Aldehyde dehydr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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1008R0N1
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                                                                                        MEDLINE=2288257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MILLE & Reingold E.A., Grouse L.H., Derge J.G.,

MALSCHIL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max.S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

M. Diatchenko L., Warusina K., Parmer A.A., Rubin G.M., Hong L.,

M. Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Worley M., Young A.C., Shevchenko Y., Boutfard G.G.,

M. Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

M. Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M. Marra M.A.,

M. Schalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Generation and initial analysis of more than 15,000 full-length human

mouse GDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Xu C.S., Li W.O., Li Y.C., Wang L., Wang S.F., Han H.P., Wang G.P.,
Chai Li.O., Yuan J.Y., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY322227; AAP926281; --
GO; GO:0005759; C:mitochondrial matrix; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREPAMS; TIGRO1236; DipyrScarbox1; 1.
PROSITE; PSO0070; ALDEHYDE DEHYDR CYS; UNKNOWN 1.
PROSITE; PSO0687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
SEQUENCE 563 AA; 61733 ÑW; D5ADC4DA27C5B0E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 GAVFSQDKDVVQEATKVLRNAAGNFYINDK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1465 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Placenta;
       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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Matches

RESULT 4 Q7TP27

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OBBXM3
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUB=Liver;

MEDLINE=22388257; PubMed=1247392;

Altschul S.F.; Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F.; Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F.; Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F.; Zeeberg B., Buetow K.H., Schemer N.K.,

A plachenko L., Marusina K., Farmer A.A.; Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A.; Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toochiyuki S., Garvia A.M., Gaay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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McD. Mc1:2443843, AA924433.1, -.
McD. Mc1:2443883, AA930035F14Rik.
C. GO, GO:005739; Cimitochondrion; IDA.
InterPro: IPR005931; DipyrScarbox1.
Rem: PR0012086; Jaldehyde Gahydr.
Rem: PR00117; Aldedh; 1.
PR03ITE; PS00070; ALDEHYDE DEHYDR CYS; UNKNOWN 1.
RP03ITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
RP03ITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
RP03ITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
RS03ITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
RS03ITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
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                                                                                                                                                        Score 123; DB 2; Length 30. Pred. No. 1.9e-08; Pred. Totals 2; Indels
                                                                                                                         381 AA; 41755 MW; AC120FC168A5AC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMN-2002 (TYEMBLrel. 21, Created)
01-JUN-2002 (TYEMBLrel. 21, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Aldh4al protein (Fragment).
Name=A930035Fi4Rik; Synonyms=Aldh4al;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN 1.
NON TER 1 1 1 SEQUENCE 381 AA; 41755 MW; ACIZOFCI68A5AC52 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 AA
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                                                                                                                                                                                          78.8%;
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STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                               Query Match
Best Local Similarity 76.7*

These 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.7
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                               298
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98 R182

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90 CO B
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STRAIN=CS7BL/6J; TISSUE=Retina; MEDLINE=2049314; PubMed=11042159; MEDLINE=2049314; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-GSTBL/64; TISSUE-Retina;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAN=CSPBL/6J; TISSUE=Retina;
STRAN=CSPBL/6J; TISSUE=Retina;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation (
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                             QBEXM3;
01-MRA-2003 (TrEMBLrel. 23, Created)
01-MRA-2003 (TrEMBLrel. 23, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930035F14 product:ALDEHYDE DEHYDROGENASE 4 FAMILY, MEMBER A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20530913; PubMed=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamocto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikki integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Buthezia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB=Retina;
MEDLINE-9927923; Pubmed-10349636;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
||||:||||:|||||:
466 GAVFAQDKAIVQEATRMLRNAAGNFYINDK 495
                                                                                                                           562
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CSDEL/66; TISSUE=Retina;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                      homolog.
Name=A930035F14Rik;
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SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Kidney;

X ALSUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Kidney;

X Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Lacchul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lacchul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Dischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Drownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Ginbs R.A.,

Rheby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., TOuchman J.W., Green E.D., Dickson M.C.,

RA Adriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Adriguez A.C., Grimwood J., Smallus D.E., Schnerch A., Schein J.E.,

RA Adra Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse GDNA schlaus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 78.8%; Score 123; DB 2; Length 562; Local Similarity 76.7%; Pred. No. 2.9e-08; les 23; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Aldehyde dehydrogenase 4 family, member Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
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STRAIN-FVB/N; TISSUE=Kidney;
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MEDINE-22388257; PubMed=12477932;

MILLINE-22388257; PubMed=12477932;

MILLINE-22388257; PubMed=12477932;

MILLINE-22388257; PubMed=12477932;

MILLINE-22388257; MILLINE MAY S.L., Shenmen C.M., Schuler G.D.,

MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MALSCHUL S.F., Jedan H., Moore T., Max S.L., Wabin G.M., Hong L.,

MALSCHUL M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MALSCHUL S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

MILLIAIOn D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

MALSCHUL S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

MILLIAION D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

MALSCHUL S., Morley M., Touchman J.W., Green B.D., Dickson M.C.,

MALSCHUL S., Malschul S., Shevchenko Y., Bouffard G.G.,

MALSCHUL S., Malschul S., Schnutz J., Myers R.M., Butterfield Y.S.,

MILLINE S., MILL S., Schleit J.E., Schnerch A., Schein J.E.,

MALSCHULL S., Malschul S., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human "Generation and initial analysis of proce CDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=zgc:63592,
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyprinidae; Danio.
NCBL TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Whole body;
Strausberg R.;
Gol. 00005759; C:mitochondrial matrix; IEA.
GO; GO:0003842; F:1-pyrroline-5-carboxylate dehydrogenase act.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0006561; P:proline biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                   Length 562;
                                                                                                                                                                                                                                                                   Query Match 78.8%; Score 123; DB 2; Length 56 Best Local Similarity 76.7%; Pred. No. 2.9e-08; Matches 23; Conservative 5; Mismatches 2; Indels
EMEL, BCOS6226; AHIS6226.1; -..
MGD; MGI:2443883; A930035F14Rik.
GG; GO:005739; C:nitochondarion; IDA.
InterPro; IPR002081; DipyrScarbox1.
InterPro; IPR002931; DipyrScarbox1.
IIGERAMS; TIGR01236; DipyrScarbox1; 1.
TIGRFAMS; TIGR01236; DipyrScarbox1; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_GLU; UNKNOWN 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN 1.
SEQUENCE 562 AA; 61810 MW; OAFBF3FAAOC9C367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Similar to aldehyde dehydrogenase 4 family, member Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 AA.
                                                                                                                                                                                                                                                                                                                                                                                          2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
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Interpro; IPR005931; Dipyr5carbox1.
Interpro; IPR001547; Glyco_hydro_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7SY23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
Q7SY23
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=56636;
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Matches
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                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Probable delta-1-pyrroline-5-carboxylate dehydrogenase (BC 1.5.1.12)
(P5C dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PR745;
MEDLINE=98162722; PubMed=9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                 ô
                                                                                                   71.2%; Score 111; DB 2; Length 556; 66.7%; Pred. No. 1.3e-06; ive 5; Mismatches 5; Indels
Pfam; PF00171; Aldedh; 1.

TIGRPAMs; TIGR01236; Dlpyr5carbox1; 1.

PROSITE; PS00070; ALDEHYDE DEHYDR.CLU; UNKNOWN 1.

PROSITE; PS00687; ALDEHYDE DEHYDR—GLU; UNKNOWN—1.

PROSITE; PS00659; GLYCOSYL HYDROL F5; UNKNOWN 1.

SEQUENCE 556 AA; 61587 WW; E7973E9787CEA358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                548 AA.
                                                                                                                                                                            2 GAVFSQDKDVVQEATKVLRNAADNFYINDR 31
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                                                                                                                    66.78;
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    ORFNames=SPBC24C6.04;
                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
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                                                                                                                                                                                                                                     RESULT 10
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MEDLINE=99310339; FUNNEW=103200;
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
HOSOYMAR A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
HOSOYMAR A., Rushida S., Funnahashi T., Tanaka T., Kudoh Y.,
Takamiya M., Mushida N., Oguchi A., Aoki K.-I., Kudoh Y.,
Takamiza Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
BNR: AP2673; AP2673.
GO; GO:0005759; C:mitochondrial matrix; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K -> N (in Ref. 2)
E -> G (in Ref. 2)
E -> G (in Ref. 2)
F -> Y (in Ref. 2)
S -> Y (in Ref. 2)
S -> Y (in Ref. 2)
S -> L (in Ref. 2)
S -> L (in Ref. 2)
S -> L (in Ref. 2)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOX-2004 (TrEMBLrel. 26, Last annotation update)
553aa long hypothetical delta-1-pyrroline-5-carboxylate
                                                                                                                                                                                                                                                              EMBL, AL031786; CAA21148.1; --
EMBL, D89230; BAA13891.1; --
InterPro; IPR002036; Aldehyde dehydr.
InterPro; IPR002036; Aldehyde.
ITGRFAMS; TIGR01304; BADH; 1.
TIGRFAMS; TIGR01304; BADH; 1.
TIGRFAMS; TIGR01304; BADH; 1.
FROSITE; PS000687; ALDEHYDE DEHYDE CX; 1.
FROSITE; PS00687; ALDEHYDE DEHYDE CX; 1.
FROMFLICT 2000 230 298 By similarity.
CONFLICT 210 210 N > F (in Ref. 2).
CONFLICT 233 274 FR > IC (in Ref. 2).
CONFLICT 233 274 FR > IC (in Ref. 2).
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| 65 GSIFAQDRVVVRKLTDRLRNAAGNFYINDK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GAVESODKDVVQEATKVLRNAADNFYINDR 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 96;
60.0%; Pred. No. C
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MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60218 MW;
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                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor
(EC 1.5.1.12) (PSC dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Demais S., Gavrias V., Scazzocchio C.;
"Primary structure of the nuclear prnC gene involved in the mitochondrial pathway for proline utilization in Aspergillus midulans.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: 1-pyrroline-5-carboxylate + NAD(+) + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-glutamate + NADH.
--- PATHWAY: Conversion from proline to glutamate; second step.
--- SUBCELFULAR LOCATION: Mitochondrial matrix.
---- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion (Potential).
Delta-1-pyrroline-5-carboxylate
dehydrogenase.
NAD ADP part) (By similarity).
By similarity.
By similarity.
Wy 1EB410940931C71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emericella nidulans (Aspergillus nidulans).
Eukaryota, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%; Score 89; DB 1; Length 572; 60.7%; Pred. No. 0.0015; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF252630; AAF72527.1; -.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR005931; DipyrScarbox1.
Pfam; PF00171; Aldedh; 1.
TIGRFAMS; TIGR01804; BADH; 1.
TIGRFAMS; TIGR01236; DipyrScarbox1; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00689; ALDEHYDE_DEHYDR_CYS; 1.
Mitochondrion; NAD; Oxidoreductase; Proline metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 AA.
                                                                               480 GAVFSQDKEFLYRARDVLRDAVGNMYLNDK 509
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5; Mismatches
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                                          2 GAVFSODKDVVQEATKVLRNAADNFYINDR
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01-OCT-2000 (TrEMBLrel. 15, Created)
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Best Local Similarity 60.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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320
354
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320 3
354 3
572 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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GO; GO:0003842; F:1-pyrrolline-5-carboxylate dehydrogenase act. . .; IEA. GO; GO:0004541; F:oxidoreductase activity; IEA. GO; GO:0008152; P:metabolism; IEA. GO; GO:0006512; P:metabolism; IEA. InterPro; IPR002086; Aldehyde dehydr. InterPro; IPR002086; Aldehyde dehydr. InterPro; IPR002086; Aldehyde dehydr. TIGRFAMS; TIGR01236; Dipyr5carbox1. 1. PROSITE; PS00070; ALDEHYDE DEHYDR CYS; UNKNOWN 1. PROSITE; PS00070; ALDEHYDE DEHYDR GLU; UNKNOWN 1. COmplete protecome; Hypothetical protein. SEQUENCE 553 AA; 63198 MW; 767EF123A152F461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A mactarioum.";

Direct Submission.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AFO16672; AAB66116.3;

REMEL, AFO16672; AAB66116.3;

RO, GO:0003842; F:1-pyrroline-5-carboxylate dehydrogenase act...;

RO, GO:0016491; F:oxidoreducase activity; IEA.

RO, GO:0016491; F:oxidoreducase activity; IEA.

RO, GO:0008152; F:metabolism; IEA.

RO, GO:0008152; F:metabolism; IEA.

RICEPTRO, IPRO102066; Aldehyde_dehydr.

RICEPTRO, ITGRO1031; DipyrScarbox1, 1.

RIGRAMs, TIGRAD156; DipyrScarbox1, 1.

ROSITE; PSO10687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.

RYPOTHETIS, PSO10687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                        57.7%; Score 90; DB 2; Length 553; 53.3%; Pred. No. 0.001; ive 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 563;
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56.7%; Pred. No. 0.0014;
ive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Wilson R., Pauley A., Maggi L., Harper M.;
"The sequence of C. elegans cosmid F55D12.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2001 (TrEMBLrel. 18,
01-MAR-2004 (TrEMBLrel. 26,
HYPOTCHAICAL PROTEIN.
ORFNAMMES=FS6D12.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.3
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            016648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     None;
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016648
AC 016648
AC 01-0564
DT 01-0764
DT 01-0764
DT 01-076
DT 01-
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Gaps

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STRAINSATCC 10895;
Didetrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A., Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A., "The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
Saccharomyces Associate (2004).
AGD; AALO71C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                       Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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Interpro; IPR005931; DipyrScarbox1.
PIGRAM; PR00171; Aldedh; 1
PIGRFAMS; TIGR01236; DipyrScarbox1; 1.
PR0517E; PS00570; ALDEHYDE DEHYDR. GLU; UNKNOWN 1.
PRO517E; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
SEQUENCE 573 AA; 62967 WW; 300B396AB343COCZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO1236, Dlpyr5carbox1; 1.
PROSITE; PS00070; ALDEHYDE DEHYDE CAS; UNKNOWN 1.
PROSITE; PS00687; ALDEHYDE DEHYDE CLU; UNKNOWN 1.
SEQUENCE 560 AA; 61899 WW; E0C9A49DEE598536 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
02-MAR-1-cyroline-5-carboxylate dehydrogenase.
0RFNames-Chr3 0160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        075E29;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
AAL071Cp.
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                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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Best Local Simi
Matches 16;
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     ACCOCCOS ON THE STATE OF THE ST
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Query Match 55.8%; Score 87; DB 2; Length 573;
Best Local Similarity 53.3%; Pred. No. 0.0028;
Matches 16; Conservative 7; Mismatches 7; Indels 0; Gaps
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8 8

Search completed: November 10, 2004, 12:27:08 Job time : 36.9182 secs

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Fri Nov 12 14:54:50 2004
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RESULT 2
US-08-923-856-3
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Appli
                                                                                                    November 10, 2004, 11:41:17; Search time 9.8287 Seconds (without alignments) 222.664 Million cell updates/sec
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Sequence 2
Sequence 2
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1: /cgT2_6/prodata1/iaa/5A_COMB.pep:*
2: /cgT2_6/prodata/1/iaa/5B_COMB.pep:*
4: /cgT2_6/prodata/1/iaa/6A_COMB.pep:*
5: /cgT2_6/prodata/1/iaa/6B_COMB.pep:*
6: /cgT2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/prodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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171
1 TGTGAPRFIKEVQELNSALHQSDLIDIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                      Run on:
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45, ADD
13, ADD
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4822, AD
6448, AD
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                 US-09-091-814-45
US-09-124-611-13
US-08-805-965-1
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US-09-252-991A-31538
US-09-583-110-4822
US-09-134-000C-6333
US-09-134-00C-6448
US-09-613-99C-6448
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US-09-149-476-6296
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| Patent No. 5928894
| GENERAL INFORMATION:
| APPLICANT: Lal, Preeti
| APPLICANT: Tang, Tom
| APPLICANT: Tang, Tom
| APPLICANT: Shah, Purvi
| TITLE OF INVENTION: HUWAN ACTVA-ORF4-LIKE PROTEIN
| NUMBER OF SEQUENCES:
| ADDRESSEE: Incyte Pharmaceuticals, Inc.
| STREET: 3174 Porter Dr.
| CITY: Paio Alto
| COUNTRY: USA
| COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

34.5%; Score 59; DB

Best Local Similarity 48.0%; Pred. No. 2;

Matches 12; Conservative 5; Mismatches
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> LOCATION: (0) ...(0)

> CHARL INNEATION: Polypeptide Accession Number P52756

US-09-538-092-1196
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
31.9%; Score 54.5; D:
Best Local Similarity 52.2%; Pred. No. 4.9;
Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GAPRFIKEVOELNSALHOSDLID 26
                                                                                       294 amino acids
                                               SEQUENCE CHARACTERISTICS LENGTH: 294 amino acid
              INFORMATION FOR SEQ ID NO:
                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                     TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GenBank CLONE: 46816
                                                                                                                TYPE: amino acid
STRANDEDNESS: siz
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US-09-538-092-1196
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Sequence 3, Application US/09216294

Patent No. 6080723

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Tang, Tomig, Towig, Towig,
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCHWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,856
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,294
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/923,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.9%; Score 54.5; Dilarity 52.2%; Pred. No. 4.9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0380 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-855-0555
IELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
IYPE: amino acids
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0380 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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ATTORNEY/AGENT INFORMATION:
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LIBRARY: Genbe
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ZIP: 94304
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US-08-923-856-3
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Sequence 20666, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409
Sequence 1196, Application US/09538092

Sequence 1196, Application US/09538092

Sequence 1196, Application US/09538092

GENERAL INFORMATION:

APPLICANT: Glot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CLIRAPALSGFORMATER VETSION 0.9
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LENGTH: 224

RESULT 6 US-09-710-279-1210

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Sequence 4343, Application US/09134001C

Sequence 4343, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 4343
LENGTH: 560
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Sequence 2832, Application US/09710279

Pacent No. 6703492

GENERAL INFORMATION:

APPLICATURY KIMMERLY, WILLIAM JOHN

TITLE OF INVERTION: STAHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 1200-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2832

LENGTH: 584

TYPE: PRT

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) OTHER INFORMATION: Description of Artificial Sequence: synthetic
) OTHER INFORMATION: amino acid sequence
19.09-710-279-2832
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Best Local Similarity 40.0%; Pred. No. 34;
Matches 10; Conservative 6; Mismatches 5
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15 XWNEIMEALEQSELIIHRHLRP 37
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GENERAL INFORMATION:
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Best Local Similarity 40.0
Matches 10; Conservative
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US-09-710-279-2832
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US-09-520-822A-4
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Sequence 3789, Application US/09134001C

Extent No. 6380370

GENERAL INFORMATION:

TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PLING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-14-08

DRIOR FILING DATE: 1997-16-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3789

LENGTH: 323

TYPE: PRT

CORGANISM: Staphylococcus epidermidis

US-09-134-001C-3789
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Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1210
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                                                                                                                                                                         Score 51; DB 4; Length 224;
Pred. No. 12;
2; Mismatches 6; Indels
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ORGANISM: Artificial Seguence
                                                                                                                                                                         Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                    ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20686
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RESULT 7 US-09-134-001C-3789

FEATURE:

Query Match Best Local Similarity Matches 11; Conserva

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APPLICANT: Chen, Xiaojiang
TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
FILE REFERENCE: Harvard/Harrison 12687/1120
CURRENT PEPLICATION NUMBER: US/09/520,822A
CURRENT FILING DATE: 1990-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: HOMOURE et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: ParentIn Ver. 2.0

SEQ ID NO 49721

LENGTH: 219
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Sequence 34504, Application US/09270767

Sequence 34504, Application US/09270767

Sequence 34504, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

TILLE OF INVENTION: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 34504

LENGTH: 219
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29.5%; Score 50.5; DB 4; Length 462;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 12; Conservative 4; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34504
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human papillomavirus type 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Drosophila melanogaster
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ORGANISM: Drosophila melanogaster
FEATURE:
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US-09-270-767-49721
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Sequence 3351, Application US/09134001C

Facent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: DATE: 1998-08-13

PRICE APPLICATION NUMBER: US 60/064,964

PRICE APPLICATION NUMBER: US 60/064,964

PRICE RILING DATE: 1997-08-14

PRICE PLING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3351

LENGTH: 249
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APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1099-11.09
NUMBER OF SEQ ID NOS: 4472
SSOFTWARE: Patentin Ver: 2.1
SSOFTWARE: Patentin Ver: 2.1
LENGTH: 241
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                                                                         Length 219;
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                                                                    29.2%; Score 50; DB 4; llarity 33.3%; Pred. No. 16; Conservative 7; Mismatches
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 KLNDLNDRLTMHHMDLKDVYQTFQP 110
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                                                                                                                                                                                                     110 TGXGSPRFVEKXSASESVTYYADI 133
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US-09-134-001C-3351
                                                                                                                                                                                                                                                                                                                    US-09-710-279-856
; Sequence 856, Application US/09710279
; Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
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US-09-134-001C-3351
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RESULT 15

US-09-540-216-2594

US-09-540-216-2594

FORDER DEPOSED TO THE PROPERTY OF THE PROPERTY OF THE PARTING TO MORAXELLA CATARY TITLE OF INVENTION: NUCLEIC ACID. AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARY TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: US/09/540,236

LENGTH: 260

LENGTH: 260

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

COGANISM: M.catarrhalis

US-09-540-236-2594
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Best Local Similarity 39.1%; Pred. No. 28;
Matches 9; Conservative 6; Mismatches 8; Indels
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Search completed: November 10, 2004, 12:32:27 Job time : 9.8287 secs

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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Sequence 143, App
Sequence 43729, A
Sequence 2058, Ap
Sequence 2058, App
Sequence 210336,
Sequence 2, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 1034, A
Sequence 1071,
Sequence 1758, A
Sequence 17728, A
Sequence 17728, A
Sequence 22036, A
Sequence 2336, A
Sequence 2181, Ap
Sequence 22036, A
Sequence 22036, A
Sequence 22036, A
Sequence 23634, A
Sequence 23634, A
Sequence 23634, Sequence 23634, Sequence 21100, A
Sequence 21100, A
Sequence 259701, Sequence 21100, A
Sequence 259701, Sequence 12, Appli
Sequence 13, Appli
Sequence 12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
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| Sequence 14, Application US/10092750 |
| Publication No. US2003003157A1 |
| GENERAL INPORMATION: |
| APPLICANT: Hammond, Philip W. |
| APPLICANT: Wright, Martin C. |
| TITLE OF INVENTION: POlypeptides Interactive with BCL-X1 |
| FILE REFERENCE: 50036/050002 |
| CURRENT APPLICATION NUMBER: US/10/092,750 |
| CURRENT FILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 2001-03-08 |
| NUMBER OF SEQ ID NOS: 253 |
| SOFTWARE: PastSEQ for Windows Version 4.0 |
| SEQ ID NO 14 |
| TYPE: PRT |
| TYPE: PRT |
| CRGANISM: Homo sapiens |
| US-10-092-750-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                       Query Match
100.0%; Score 171; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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; Publication No. US20030064377A1
; GENERAL INFORMATION:
     RESULT 2
US-10-012-600B-221
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Sequence 221, App
Sequence 25, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 34, Appl
Sequence 34896, A
Sequence 34896, A
Sequence 31728, A
Sequence 7728, A
                                                                                          November 10, 2004, 15:53:52; Search time 31.8287 Seconds (without alignments) 366.225 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/PGT_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PGT_BW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PGT_BW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NBW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USOF_NBW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USOF_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USIOF_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-012-6008-221

4 US-10-022-8238-357

4 US-10-025-201-3

5 US-10-114-270-30

6 US-10-114-55-850

6 US-10-145-615-3

6 US-10-145-615-3

6 US-10-145-615-3

6 US-10-145-615-3

7 US-09-84-761-34496

4 US-10-106-698-4989

4 US-10-106-698-4989

6 US-10-106-698-4989

7 US-09-84-761-3486

7 US-09-84-761-3486

7 US-09-84-4087-7726

7 US-09-84-4088-31728

8 US-10-108-2608-4488
                                                                                                                                              US-10-092-750-14
171
1 TGTGAPRFIKEVQELNSALHQSDLIDIYRTLHP 33
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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1031
1272
1272
1274
1274
167
167
110
110
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Gaps

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Score

Result

171 125.5 125.5 125.5 125.5 116.5 116.5 116.5 72.5 72.5 67

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APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110Alel Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: MARKERS FOR DISEASE SUSCEPTIBILITY AND TARGETS FOR THERAPY FILE REFERENCE: 5983/24567
CURRENT APPLICATION NUMBER: US/10/025,201
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,673
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
LENGTH: 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----OELNSALHOSDLI 25
                                                                                                                                                                                                                                                                                                                 DATABASE ACCESSION WIMBER: GenBank Accession No. US20030003468A1 U09116
DATABASE ENTRY DATE: 1995-02-02
RELEVANT RESIDUES: (1)..(1275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                73.4%; Score 125.5; DB 14; Length 1275; 42.6%; Pred. No. 3.28-09; tive 2; Mismatches 0; Indels 37;
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CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
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Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
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PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-114-270-30
'Sequence 30. Application US/10114270
'Publication No. US20040030110A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenoy, Suresh G.
Pena, Carol E.A.
Smithon, Glennda
Burgess, Catherine E.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ji, Weizhen
Anderson, David W.
Liete, Marlo W.
Rastelli, Luca
Edinger, Shlomit R.
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Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu, Ziaohong
Susev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGAPRFIKEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.6
Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vernet, Corine
                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 DİYRTLHP 186
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APPLICANT:
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APPLICANT:
APPLICANT:
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Sequence 257, Application US/10082828A

Sequence 257, Application US/10082828A

Sequence 257, Application US/10082828A

Publication No. US20030175715A1

SERVERAL INFORMATION:

APPLICANT: Salveda, Susana

APPLICANT: Leah

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr

TITLE OF INVENTION NUMBER: US/10/082,828A

CURRENT FILING DATE: 2000-07-09

PRIOR FILING DATE: 2000-10-27

NUMBER OF SEQ ID NOS: 266

SOFTWARE: PatentIn Version 3.1

LENGTH: 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ᅜ
       APPLICANT: Sun, Yongwing
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yon, Herve
APPLICANT: Chen, Sei-Yon, Herve
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX. 0265
CURRENT APPLICATION NUMBER: US/10/012,600B
CURRENT FILING DATE: 2001-11-06
PRIOR FLIANG DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Version 3.1
SEQ ID NO 221
LENGTH: 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 TGAPRFIKQVLSDLQRDLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.4%; Score 125.5; DB 14; Length 1031; Best Local Similarity 42.6%; Pred. No. 2.5e-09; Matches 29; Conservative 2; Mismatches 0; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125.5; DB 14; Length 363;
Pred. No. 7.1e-10;
2; Mismatches 0; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-025-201-3
Sequence 3, Application US/10025201
Publication No. US2003003468A1
CENERAL INFORMATION:
APPLICANT: Crow, Mary K.
                                                                                                                                                                                                                                                                                                                                                                                                                      73.48;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TGAPRFIKEV---
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                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-600B-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 DIYRTLHP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-10-082-828A-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 DIYRTLHP 33
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 998
SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 850—
LENGTH: 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc feature
; CTHER INFORMATION: Incyte ID No: 1258887CD1
US-10-415-615-3
                                                                                                                                                                                                                                                                                                                                                                                                                           10 KEVQELNSALHQSDLIDIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TGAPRFIKEV-----
                                                                                                                                                                        rype: PRT
CORGANISM: Homo sapiens
US-10-243-552-850
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ORGANISM: Homo sapiens
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   PRIOR FILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR APPLICATION NUMBER: 60/283,130
PRIOR PILING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-17
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APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezin
APPLICANT: Weng, Gezin
APPLICANT: Weng, Gezin
APPLICANT: Weng, Gezin
APPLICANT: Weng, Gezin
APPLICANT: Weng, Cezin
APPLICANT: Ma, Yunqing
TITLE OF INVENTION: Dovel Nucleic Acids and
TITLE OF INVENTION: Dovel Nucleic Acids and
TITLE OF INVENTION: Dovel Number: US/10/243,552
CURRENT APPLICATION NUMBER: US/10/243,552
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-02-03
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Publication No. US20030224379A1
GENERAL INFORMATION:
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Best Local Similarity 41.2
Matches 28; Conservative
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US-10-114-270-30
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LENGTH: 1272
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                                                                        Gaps
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Query Match 67.8%; Score 116; DB 14; Length 936; Best Local Similarity 87.5%; Pred. No. 5.6e-08; Matches 21; Conservative 3; Mismatches 0; Indels C
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US-101-104-047-2288
US-10-104-047-2288
Sequence 2288, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
                                                                                                                                                                                                                                                                                                                                               US-10-415-615-3

US-10-415-615-3

US-10-415-615-3

US-10-415-615-3

US-10-415-615-3

US-10-415-615-3

US-20-40-10-19-30-1

US-20-40-10-19-30-1

GENERAL INFORMATION:

APPLICANT: BAUGHN, Mariah R.

APPLICANT: VUC, Yan

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: PAFALIA, April J.A.

APPLICANT: LAL, Preet G.

TITLE REFERENCE: Preet G.

TITLE REFERENCE: Preet G.

TITLE REFERENCE: PLO280 USN

CURRENT APPLICATION NUMBER: US 60/245,458

PRIOR FILING DATE: 2000-11-02

PRIOR FILING DATE: 2000-11-12

PRIOR PRIOR APPLICATION NUMBER: US 60/255,107

PRIOR FILING DATE: 2000-11-12

PRIOR FILING DATE: 2000-11-12

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PERL PROGRAM

SEQ ID NO 3

LENGHH: 1274
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 34496 LENGTH: 167
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48.5%; Score 83; DB 14; L
Best Local Similarity 70.8%; Pred. No. 0.00022;
Matches 17; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 PKVNKETMDLNYTLEQMDLTDIYRTFHP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PRFIKEVQELNSALHQSDLIDIYRTLHP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4989, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 4989
LENGTH: 79
                                                                                                                                                                     OTHER INPORMATION: MAP TG
OTHER INPORMATION: EXPRES
OTHER INPORMATION: EXPRES
OTHER INPORMATION: EXPRES
OTHER INPORMATION: EXPRES
OTHER INPORMATION: EXPRES
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OTHER INPORMATION: EXPRES
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OTHER INPORMATION: EXPRES
OTHER INPORMATION: EXPRES
                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-10-106-698-4989
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APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Acomica-X-1
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     ; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR PELICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTHARE: Patentin Ver. 2.1
; SEQ ID NO 2288
; LENGTH: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/32,366
PRIOR APPLICATION NUMBER: US 60/33,359
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00665
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-104-047-2288
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Sequence 31728, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides TILE REPERENCE: PAGOSPI CURRENT APPLICATION NUMBER: US/10/106,698 CURRENT FILING DATE: 2002-03-27 PRIOR PAPLICATION NUMBER: PCT/US/00/26524 PRIOR PAPLICATION NUMBER: US 60/157,137 PRIOR FILING DATE: 1999-09-29 PRIOR FILING DATE: 1999-09-29 PRIOR FILING DATE: 1999-11-03 PRIOR FILING DATE: 1999-11-03
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HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
HER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.5
HER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.5
HER INFORMATION: SYSTEMAN HIT: AMS67328.1, BYALUE 4.00e-59
HER INFORMATION: SWISSPROT HIT: PO8548, EVALUE 1.00e-51
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APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sel-Yu
APPLICANT: Chen, Sel-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and I
FILE REPERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2000-11-01
PRIOR PAPLICATION NUMBER: 60/244,782
PRIOR PILING DATE: 2000-11-01
SOFTWARE: Patentin version 3.1
SEQ ID NO 143
LENGTH: 230
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APPLICANT: Elach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Encoc PILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/99/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
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                                                                                         ; Sequence 4489, Application US/10108260A; Publication No. US20040005560A1; Publication No. US20040005560A1
; GENERAL INKORMATION:
; APPLICANT: HELLX RESEARCH INSTITUTE
; TILLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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Pred. No. 0.094;
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Pred. No. 0.73;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 143, Application US/10000256A; Publication No. US20030039983A1; GENERAL INFORMATION:
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11 KKTLDLNATLDQMDLTDIXRTVY 33
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Best Local Similarity 52.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.4°
                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-260A-4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapien
US-10-000-256A-143
                                                    RESULT 13
US-10-108-260A-4488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-864-408A-8046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-000-256A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
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Publication No. US200400094741

Publication No. US200400094741

APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encornance of Invention Number: US/09/864,408A

CURRENT APPLICATION NUMBER: US/09/864,408A

CURRENT FILING DATE: 2001-05-24

PRICR APPLICATION NUMBER: 60/206,690

PRICR ILING DATE: 2000-05-24

NUMBER: OF SEQ ID NOS: 9068

SCO ID NO 7726

SEQ ID NO 7726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (16)7. (16)
OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (22)...(22)
OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (104).. (104)
OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72.5; DB 14; Length 110;
Pred. No. 0.012;
8; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.4%; Score 69; DB 11; Length 114; Best Local Similarity 65.0%; Pred. No. 0.041; Matches 13; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AL117259.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14

COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 14

COTHER INFORMATION: SHISSPROT HIT: POBS47, EVALUE 2.00e-12
US-10-029-386-31728
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 31728
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 KEVQELNSALHQSDLIDIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:::|| : ::| ||:|||||:|
59 KDIEELKNTINQ-DLVDIYRTLYP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ELNSALHQSDLIDIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcn 42.4%;
al Similarity 54.2%;
13; Conservative 6
                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-864-408A-7726
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PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8046

LENGTH: 99

TYPE: RRT

CRGANISM: Homo sapiens

FEATURE:
NAMPSKEY: misc feature

LOCATION: (11)...(11)

COTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid

US-09-864-408A-8046
```

Qy 9 IKEV--QELNSALHQSDLIDIYRTLHP 33 ||:::||:::||:|| | 70 IKKIRTBELNNTINQTYLISLYRILYP 96

1;

2; Gaps

Query Match 35.1%; Score 60; DB 11; Length 99; Best Local Similarity 44.4%; Pred. No. 0.74; Matches 12; Conservative 9; Mismatches 4; Indels

Search completed: November 10, 2004, 16:35:58 Job time : 40.8287 secs

```
GenCore version 5.1.6 (c) 1993 ~ 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

November 1.0, 2004, 11:36:51; Search time 6.6713 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-14

171 1 TGTGAPRFIKBVQELNSALHQSDLIDIYRTLHP 33 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	retrovirus-relate	line-1 protein ORF	reverse transcript	trans	cal	retrovirus-related	pol	ě	B-re	hypothetical prote			B	hypothetical prote	1		maltose ABC transp	elicase	hypothetical prote	L2 protein - human	flagellar biosynth	flagellar biosynth	otein	collagen alpha 2(V	collagen alpha 2(V	cal	hypothetical prote	cal	5
		GNHUL1	B28096	I38588	\sim	B34087	GNLRL1	821346	516788	GNMSLL	F69805	S18542	T21973	S77850	E70798	836565	D71288	H72282	T38130	F82385	P2WL18	09906Н	F85511	F64747	\$23377	504111	A81387	T50469	A25657	
	DB		~	~	N	~	4	0	7	н	7	N	~	~	N	N	7	N	~	2	-1	Ŋ	N	~	N	~	~	7	~	,
	gth	1259	1275	1275	1275	1280	1260	202	500	1281	407	294	501	178	448	463	518	823	944	292	462	579	579	579	918	1022	111	710	710	
* 2	Match	73.4	m	73.4	ω.	m		ů,	'n	ω.	ď	Ή.	급.	н	ö	30.4	。	29.8	6	σ.	٥.	6	σ.	φ.	ο.	ď	ο,	ď	φ.	
	COL	25	25	125.5	25	25	78	62	60.5	57	55	54.5	54	53.5	52.5	52	51.5	51	51	0	0	0	50.5	0	0	0	50	20	20	1
	No.		N	٣	4	Ŋ	φ	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	•

GPI-linked recepto	probable flavin-co	cartilage oligomer	RNA-directed RNA p	3-methyl-2-oxobuta	MHa2 (keratin acidi	conserved hypothet	MADS-box protein -	exodeoxyribonuclea	probable membrane	translation releas	conserved hypothet	citrate (pro-3S)-1			hypothetical prote
JE0082	A83453	A44315	WMWGPV	T47119	I48739	F89858	T09700	H83327	C72492	B81257	F81674	G86773	T18941	T39808	H84522
~	~	7	Н	N	N	N	N	~	N	~	N	~	7	7	7
397	527	755	1456	271	407	127	240	270	283	355	369	512	1551	1958	386
28.7	28.7	28.7	28.7	28.4	28.4	28.1	28.1	28.1	28.1	28.1	28.1	28.1	28.1	28.1	27.8
49	49	49	4	48.5	48 7	48	48	48	4.8	4.8	48	48	48	48	47.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1
GNHUL1
CARBULT 1
GNHUL1
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Sakabi. 131-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
C. Accession: A25313
R. Hattori, M.; Kuhara, S.; Takenaka, O.; Sakaki, Y.
Nature 321, 625-628, 1986
A. Title: Li family of repetitive DNA sequences in primates may be derived from a sequence A. Reference number: A93381; MulD:86230917; PMID:2423883
A. Reference number: A93381; MulD:86230917; PMID:2423883
A. Reference number: DNA
A. Reference NA
A. Residues: 1-1259 cHAT>
A. Molecula type: DNA
A. Residues: 1-1259 cHAT>
A. Molecula type: Lass constructed from an alignment of published and unpublished sequence: this sequence was constructed from an alignment of published and unpublished sequence: reverse transcriptase; pseudogene

-Gaps Match 13.4%; Score 125.5; DB 4; Length 1259; Local Similarity 42.6%; Pred. No. 6.4e-09; Nes 29; Conservative 2; Mismatches 0; Indels 37; Best Loc Matches

3 TGAPRFIKEV------QELNSALHQSDLI 25 셤 ò

178 DIYRTLHP 185 26 DIYRTLHP 33 ò qq

RESULT B28096

Line-1 protein ORP2 - human (man) () Species: Homo sapiens (man) () Species: Homo sapiens (man) () Species: Homo sapiens (man) () Species: Homo sapiens (man) () Species: Homo sapiens (man) () Singer () Singer () Sing

ä Gaps 37; Query Match

73.4%; Score 125.5; DB 2; Length 1275;
Best Local Similarity 42.6%; Pred. No. 6.5e-09;
Matches 29; Conservative 2; Mismatches 0; Indels 37; 1;

Length 1280;

25

-----OELNSALHQSDLI Indels 37; Gaps

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Cispecies: Homo sapiens (man)
Cispecies: Anomorable (man)
Cispecies: Anomorable (man)
Cispate: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
Cispate: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
Cispate: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
Riscott, A.P.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J.I.
A; Roscott, A.P.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J.I.
A; Reference number: A34087; MUID:88085185; PMID:3692483
A; Resetue: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-1280 <SCO>
A; Residues: 1-1280 <SCO>
A; Cross-references: UNIPROT:Q9YSKO
C; Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Nycticebus coucang (slow loris)
C.Jate: 31-Mar-1998 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
C.Jacession: B25313
R.Hattori, M.; Kuhara, S.; Takenaka, O.; Sakaki, Y.
Nature 311, 655-628, 1986
A.Fitle: L. I family of repetitive DNA sequences in primates may be derived from a sequence A.Reference number: A99381; MUID:86230917; PMID:2423883
A.Accession: B25313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retrovirus-related reverse transcriptase pseudogene - slow loris
                                                                                                                                                                                                                                                                                                                                                                 Score 125.5; DB 2;
Pred. No. 6.5e-09;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: conceptual translation of pseudogene A;Molecule type: DNA
hypothetical protein (L1H 3' region) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 KEILDLNSTIQHLDLTDIYRTFHP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 KEVQELNSALHQSDLIDIYRTLHP 33
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Best Local Similarity 42.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGAPRFIKEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 DIYRTLHP 191
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A;Molecule type: DNA
A;Rosicuse: 1-1275 <RES>
A;Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:g483914; PIDN:AAB60345.1; PID:g4839
C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1275 <DOM>
A;Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AAA51622.1; PID:g3397
C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q A;Reference number: 138587; MUID:95004577; PMID:7920631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                    119 TGAPRFIKOVLSDLQRDLDSHTLIMGDFNTPLSILDRSTRQKVNKDTQELNSALHQADLI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                          reverse transcriptase homolog - human retrotransposon Li
NiAlternate names: ORF2 protein
C;Spacies: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 13858
E;Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 85824
R;Dombroski, B.A.
submitted to the EMBL Data Library, January 1992
A;Bescription: Isolation of an active human transposable element.
A;Reference number: 855823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QELNSALHQSDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125.5; DB 2;
Pred. No. 6.5e-09;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 125.5; DB 2;
Pred. No. 6.5e-09;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reverse transcriptase homolog - human transposon L1.1
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Best Local Similarity 42.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.6
Matches 29; Conservative
                                                                                                                                                                   DIYRTLHP 186
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                                                                                                                    26 DIYRTLHP 33
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                       TGAPRFIKEV-
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A;Residues: 1-1260 <HAT>
A;Cross-references: UNIPROT:P08548
A;Cross-references: UNIPROT:P08548
C;Keywords: this sequence was constructed from an alignment of six sequences, determined by t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q63304; EMBL:X53581; NID:g56586; PIDN:CAA37645.1; PID:g56588
A;Experimental source: strain Wistar
C;Superfamily: pol polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable pol polyprotein-related protein 2 - rat
probable pol polyprotein-related protein 2 - rat
probable pol polyprotein-related protein 2 - rat
c;Species: Ratus norvegicus (Norway rat)
c;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21346
R;Schmitz E.; Nohr, E.
A;Reference number: S21345
A;Reference number: S21345
A;Rocession: S21346
A;Rolecule type: DNA
A;Residues: 1-202 <SCH>
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    .
0
                                                                                                                                                     Query Match
Best Local Similarity 58.3%; Pred. No. 0.024;
Matches 14; Conservative 3; Mismatches 7; Indels
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RESULT 5 B34087

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hypothetical protein yfjB - Bacillus subtilis
CjSpecies: Bacillus subtilis
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CjSpecies: Colore: O'S D. Bruschi, C.V.; Caldwell, B.; Captano, V.; Carter, N.N.; Cho;
A.; Bron, S.D.; Bruschi, C.V.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.; Abuthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, i.ch, N.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Xumano, M.; Kurita, R.; Lapidus, A.; Laudinois, A.; Authors: Laber, J.; Lazarevic, W.; B.; Parro, V.; Pon., T. I., N.; Poteetelle, Y. M.; Ogawa, K.; Ogiwara, A.; Odiwara, B.; Parrk, S.H.; Parro, V.; Ponl, T.M.; Poteetelle, Y. M.; Ogawa, K.; Ogiwara, A.; Cucher, E.; Roche, B.; Rose, M.; Sadoie, Y.; Scanlon, A,Authors: Schledich, S.; Schreder, R.; Scoffone, P.; Tognoni, M.; Tosato, V.; Uchiyama, A; Authors: Vehikawa, H.F.; Zumanoto, H.; Yamanoto, R.; Yasumoto, K.;                                                             A, Molecule Lype: mRNA
A, Residues: 1-85, 12, 87-358, 12, 360-706, 12, 708-735, 14, 737-760, 10, 762-927, 10, 929-1281
A, Cross-references: EMBL: U15647; NID: 9558906; PIDN: AAA67727.1; PID: 9558908
R; Mottez, E.; Rogan, P.K.; Manuelidis, L.
Nucleic Acida Res 14, 3119-3136, 1986
A, Title: Conservation in the 5' region of the long interspersed mouse L1 repeat: implicat
A, Reference number: A23772; MUID: 86176789; PMID: 3008107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 'NNOESNHSTNQKEDSHKNR',1-245,'K',247-423,'SYTQQNWKTWTKWTN',439,'WTDTRYQS'
A,Cross-references: GB:X03725, NID:g52829; PIDN:CAA27363.1; PID:g1334115
C,Superfamily: pol polyprotein
C,Keywords: reverse transcriptase
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hypothetical protein 4 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 13-Jan.1995 #sequence_revision 13-Jan.1995 #text_change 09-Jul-2004
C;Accession: $18542
R;Caballero, J.L.; Martinez, E.; Malpartida, F.; Hopwood, D.A.
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C,Superfamily: Bacillus subtilis hypothetical protein yfjB
A;Accession: I49130
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 1;
Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GTGAPRFIKEVQELNSALHQSDLIDIYRTL 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 KEVQELNSALHQSDLIDIYRTLHP 33
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hes 11; Conservative
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NyAlternate names: LINd repetitive element ORF-2; LINE-1 hypothetical protein; ORF 3900;
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence revision 08-Jan-1999 #text_change 09-Jul-2004
C;Accession: B58927; B24906; I49130; A23772; B23430
C;Accession: B58927; B24906; I49130; A23772; B23430
C;Accession: B58927; B24906; I49130; A23772; B23430
A;Title: The sequence of a large LIMG element reveals a tandemly repeated 5' end and sev
A;Reference number: A93072; MUD:87064284; PMID:3023821
A;Retus: translated from GB/EMBL/DDBJ
A;Residues: translated from GB/EMBL/DDBJ
A;Residues: L-1281 <LOE1-
A;Cccssion: B58927
A;Residues: UNIPROT:P11369; UNIPROT:Q60713; UNIPROT:Q61787; GB:M13002; NID:g2008
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A;Molecule type: DNA
A;Residues: 'NNOESHHSTNQKEDSHKNR', 1-1281 <LOE2-
A;Accession: B2406
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A;Cccssion: B2406
A;Molecule type: DNA
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A;Cccssion: B2406
A;Molecule type: DNA
A;Residues: 'NNOESHHSTNGKEDSHKNR', 1-1281 <LOE2-
A;Cccssion: B2406
A;Molecule type: DNA
A;Reference sequence shown in Fig. 2
A;Noce: sequence shown in Fig. 2
A;Noce: sequence shown in Fig. 2
A;Noce: sequence shown in Fig. 2
A;Note: sequence shown in Fig. 3
A;Note: sequence shown in Fig. 2
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A;Note: s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable reverse transcriptase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 516788; B44492
R;Kahre, O.; Ilves, H; Speek, M.
submitted to the EMBL Data Library, August 1991
A;Reference number: 316788
A;Accession: 51678
A;Accession: 51678
A;Accession: 51678
A;Residues: 1-500 «KMH»
A;Residues: 1-500 «KMH»
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A;Residues: 1-500 «KMH»
A;Residues: 1-500 «KMH»
A;Accession: B4492
A;Aitle: Translation of the rat LINE bicistronic RNAs in vitro involves ribosomal reinit
A;Accession: B4492
A;Accession: B4492
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Pred. No. 2.2;
5; Mismatches
          Pred. No. 0.48;
4; Mismatches
                                                                                                                                                       10 KEVOELNSALHOSDLIDIYRTLHP 33
                                                                                                                                                                                                               Query Match
Best Local Similarity 26.5%;
Matches 18; Conservative
               l Similarity 45.8%;
11; Conservative
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          Best Local Similarity
Matches 11; Conserv
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Search completed: November 10, 2004, 12:29:18 Job time : 8.6713 secs
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   2 GTGAPRFIKEVOELNSALHOSD-LIDIY
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Best Local Similarity 47.8%;
Matches 11; Conservative
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Best Local Similarity
Matches 13; Conserv
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Mol. Gen. Genet. 230, 401-412, 1991
Ayfitle: Organisation and functions of the actVA region of the actinorhodin biosynthetic
A;Reference number: S18539; MUID:92114870; PMID:1766437
A;Accession: S18542
                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <CAB>
A;Cross-references: UNIPROT:Q53906; EMBL:X58833; NID:g46812; PIDN:CAA41640.1; PID:g46816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable histidine-tRNA ligase (EC 6.1.1.21) - Mycoplasma capricolum (fragment)
NAlternate names: histidyl-tRNA synthetase; protein MC191
C;Species: Mycoplasma capricolum
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo
A;Reference number: S77739; MUID:96059641; PMID:7476192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:020179; EMBL:277660; PIDN:CAB01172.1; GSPDB:GN00022; CESP:F3
A;Experimental source: clone F38H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: Î-178 <BOR>
Cross-references: UNIPROT:Q49027; EMBL:Z33137; NID:g516219; PIDN:CAA83774.1; PID:g5304
Experimental source: ATCC 27343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F38H4.4 - Caenorhabditis elegans
C.Speciese Caenorhabditis elegans
C;Date: 15-OCt-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21973
                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Genetic code: SGC3
A;Genetic code: SGC3
C;Keywords: aminoacyl-tRWA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                  Query Match 31.9%; Score 54.5; DB 2; Length 294; Best Local Similarity 52.2%; Pred. No. 8.1; Matches 12; Conservative 5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 31.6%; Score 54; DB 2; Length 501; Local Similarity 40.0%; Pred. No. 17; onservative 7; Mismatches 5; Indels
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A; Introns: 15/1; 87/3; 203/3; 311/2; 349/2; 431/3; 460/3
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A;Residues: 1-501 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                        4 GAPRFIKEVOELNSALHQSDLID 26
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A;Accession: S36565
A;Molecule type: DNA
A;Residues: 1.463 ADED.
A;Residues: 1.463 ADED.
A;Cresidues: UNIPROT:P36761; EMBL:X74479; NID:g397022; PIDN:CAA52577.1; PID:g39702
C;Superfamily: papillomavirus L2 protein
C;Keywords: late protein
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                  C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
R.Cole, S.T., Brosch, R.; Parkhill, J.; Carnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Aslandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:982955987; PMID:9634230
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C;Species: human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36565
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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hypothetical protein Rv3740c - Mycobacterium tuberculosis (strain H37RV)
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Run on:

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November 10, 2004, 11:27:01; search time 36:1065 Seconds (without alignments) 525.871 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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171
1 TGTGAPRFIKEVQELNSALHQSDLIDIYRTLHP 33
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2: uniprot_trembl:*
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RESULT 2
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AC P08547; 1948 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 44, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

Bac86846 homo sapi Q8n7v1 homo sapien Q6qi35 rattus norv Aas6624 rattus norv Q6tug5 rattus norv Aaq91035 rattus norv Aaq91038 rattus norv Aaq91038 rattus norv Aaq96221 rattus norv Aaq96221 rattus norv Aag66285 rattus norv As66285 rattus norv	্ব জ	sed) seq) annotation update) annotation update) niata, Vertebrata, Euteleostomi, arrhini, Hominidae, Homo.	Scott A.F., insertion in an intron of the nce of open reading frames in	GenBank/DDBJ databases. s. d DNA polymerase; Transferase. D706D841DAE0DAD4 CRC64;	; DB 2; Length 1192; :6e-08; Indels 37; Gaps 1;	TGAPRFIKEVQELNSALHQSDLI 25 TGAPRFIKQVLSDLQRDLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQADLI 95	
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Indels
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SEQUENCE 1275 AA, 149201 MW; 23D516D6E4358F28 CRC64;
                                                                                                                                                                                              Created)
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                                                                                                                            Sassandan D.M., Dombooki B.A., Moran J.V., Kimberland M.L., Naas T.P., DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.; Nat. DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.; Nat. Genet. 16:37-43 (1997).

EMBL, U93563; AAC51261.1; BERD, 188096.

PIR, Bas096, Bas096.

PIR, S23650; S23650.

GO, GO:0003723; F:RNA binding; IEA.

GO, GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO, GO:000278; F:RNA-dependent DNA replication; IEA.

InterPro; IPR005135; Exc. endo_phos.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative pi50.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutèleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 37;
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1259;
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                                                                                                                                                                                                                                         PIR; A25313; GNHU1.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR00477; RVTse.
Pfam; PF00372; Exo_endo_phos; 1.
Pfam; PF00378; RVT; 1.
Direct protein sequencing; RNA-directed DNA polymerase.
SEQUENCE 1259 AA; 147112 MW; F3BC18A3803919F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d DNA polymerase; Transferase.
1275 AA; 149062 MW; 350B4F0358E525F0 CRC64;
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Pred. No. 2.8e-08;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 125.5; DB 1; st Local Similarity 42.6%; Pred. No. 2.8e-08; tches 29; Conservative 2; Mismatches 0;
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 LINE-1 reverse transcriptase homolog.
                                                                                                              MEDLINE=86230917; PubMed=2423883;
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MEDLINE=97285120; PubMed=9140393;
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Pfam; PF00078; RVT; 1.
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Best Local Similarity 42.6%;
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 DIYRTLHP 33
                 Homo sapiens (Human)
                                                            NCBI TaxID=9606;
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RNA-directed [
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                                                                                                SEQUENCE
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NEW SECURICE FROM N.A.

REQUENCE FROM N.A.

REDGINES-97285120; PubMed=9140393;

RA SASSAMAN D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,

REDGINES-97285120; PubMed=9140393;

REDGINES-97285120; PubMed=9140393;

REDGINES-97285120; Redging H.H., Jr.,

Nat. Genet. 16:37-43 (1997).

REDGINES-98096; B28096.

PIR, 2286096; B28096.

REDGINES-98096; B28096.

REDGINES-99096; B28096; B28096.

REDGINES-99096; B28096; B
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Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
Many human Ll elements are capable of retrotransposition.";
Nat. Genet. 16:37-43(1997).
EMBL; U93568; AAC51269.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----OELNSALHOSDLI
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Putative p150.
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MEDLINE-97285120; PubMed=9140393;

MEDLINE-97285120; PubMed=9140393;

A Bassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,

A DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;

T Many human L1 elements are capable of retrotransposition.";

IN Act. Genet. 16:37-43(1997).

R PIR, B28096; B28096.

PIR, B28096; B28096.

R GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0006278; F:RNA-directed DNA replication; IEA.

R InterPro; IPR00477; RVTSe.
                                                                                                                                                                                1,
                                                                                                                                                                                                                       119 TGAPRFIKOVLSDLQRDLDSHTLIMGDFNTPLSILDRSTROKVNKDTQELNSALHQTDLI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---------
                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                              0; Indels 37;
                                                                                                                                                 73.4%; Score 125.5; DB 2; Length 1275; 42.6%; Pred. No. 2.8e-08; ive 2; Mismatches 0; Indels 37;
                     GO; GO:0003723; F:RNA binding; IEA.
GO; GO:000364; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:000364; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:000578; F:RNA-directed DNA replication; IEA.
InterPro; IPR006477; RVTSe.
Pfam; PF00372; Exo endo_phos; 1.
Pfam; PF00078; RVT; I.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149077 WW; 3BBC3B2DC2E06B61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03372; Exc_endo_phos; 1.
Pfam; PF00078; RVT; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149010 MW; 588703688E7129FF CRC64;
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Last sequence update)
Last annotation update)
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les 29; Conservative
                                                                                                                                               Query Match
Best Local Similarity 42.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                  179 DIYRTLHP 186
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PIR; B28096; B28096.
PIR; S23650; S23650.
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000375
ID 00037
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PRT; 1275 AA.

PRELIMINARY;

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MEDLINE-9728510.7: Named=9140393;
Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
A Bestardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
Deberardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
In District Many human L1 elements are capable of retrotransposition.";
In Mat. Genet. 16:37-43(1997).
REMBL, U93572, AAG51276.1;
REMBL, U93572, AAG51276.1;
REMBL, U93572, AAG51276.1;
REMBL, U93572, AAG51276.1;
REMBL, U93572, AAG51276.1;
REMBL, U93572, RNA-directed DNA polymerase activity; IEA.
GO; GO:000354; F:RNA-directed DNA replication; IEA.
RICEPPO: IPR00513; Exo_endo_phos.
RICEPPO: IPR00513; Exo_endo_phos.
REMBLE PF03772; Exo_endo_phos; 1.
REMBLE PF03772; Exo_endo_phos; 1.
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EMBL; U33574; AACS1279.1; -..

PIR; B28096; B28096.

PIR; AU0033; JU0033.

PIR; S23650; S23650.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA directed DNA polymerase activity; IEA.

GO; GO:0003723; F:RNA-directed DNA replication; IEA.

InterPro; IPR005135; Exo_endo_phos.

InterPro; IPR005135; RYTSe..
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42.6%; Pred. No. 2.8e-08;
tive 2; Mismatches 0; Indels 37; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-directed DNA polymerase, Transferase.
SEQUENCE 1275 AA; 149054 MW; 456DD0F3DD7A17F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
    Created)
Last sequence update)
Last annotation update)
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Pfam; PF00078; RVT; 1.
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01-JUL-1997 (TrEMBLrel. 04. 01-JUL-1997 (TrEMBLrel. 07. 01-OCT-2003 (TrEMBLrel. 27. Putative pls0. Homo sapiens (Human)
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Best Loc Matches

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RN [1]

RX MEDINEE STOURCE FROM N.A.

RA MEDINE=97285120; PubMed=9140393;

RA Bassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,

RA DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;

RT Many human Li elements are capable of retrotransposition.";

RI Mat. Genet. 16:37-43 (1997).

BRBL, 199570; AAC51273.1; -.

DR FIR, B28086; B28086.

DR GO; GO:000364; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000564; F:RNA-dependent DNA replication; IEA.

DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.

DR InterPro; IPR00477; RVTEe.

DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.

DR Fam; PF00372; Exo endo_phos.

R Fam; PF00372; Exo endo_phos; I.

R Fam; PF00778; RVT_ I.

R NA-directed DNA polymerase; Transferase.

SQ SEQUENCE 1275 AA; 149110 MW; 4711B3BC22F7674E CRC64;
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NEDLINE=97285120; PubMed=9140393;

Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Nads T.P.,

Beneratinis R.J., Gabriel A., Swergold G.D., Kazazlan H.H. Jr.;

Tr. Mar, Human L1 elements are capable of retrotransposition.";

Nat. Genet. 16:37-43(1997).

RELIA 193567, AGAS1267.1; -.

RELIA 193567, AGAS1267.1; -.

RELIA 193567, RAS1267.1; -.

OGO, GO:0003733; FRNA binding; IEA.

GO; GO:0003733; FRNA-directed DNA polymerase activity; IEA.

GO; GO:0003735; FRNA-directed DNA replication; IEA.

RITHERPO: IPRO05135; Exo_endo_phos.

RITHERPO: IPRO05135; Exo_endo_phos.

RITHERPO: IPRO0673; RVTSe.

REAM: PF00377; RxO_endo_phos; 1.

Ream: PF00372; Exo_endo_phos; 1.

Ream: PF00078; RVT; 1.

RAM RNA-directed DNA polymerase, Transferase.

SEQUENCE 1275 AA; 149033 MW; 07E88F8F4DB831A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KEVQELNSALHQSDLI 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Gaps
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Putative p150.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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41.2%; Pred. No. 2e-07;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 121.5; DB Pred. No. 1e-07; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.1%;
Best Local Similarity 41.2%;
Matches 28; Conservative 2
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nes 28, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 DIYRTLHP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 DIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       ------QELNSALHQSDLI 25
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MEDLINE=21668188; PubMed=11810275;
Benjas S.M.;
Morris C.M.;
A full-length and potentially active LINE element is integrated polymorphically within the IGL locus in a genomically unstable region of chromosome 22.";
Hun. Genet. 109:628-637(2001).
BENBL; AF421375; AALS0637.1; -.
PIR; B28096; B28096.
PIR; S23609; S23650;
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                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OUN-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
14ypothetical protein.
16ypothetical protein.
16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 16yman | 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                 37;
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                                                                                      Length 1275;
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GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
InterPro; IPR0061315; Exo endo_phos.
InterPro; IPR000477; RVTSe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.4%; Score 125.5; DB 2; Length 42.6%; Pred. No. 2.8e-08; ive 2; Mismatches 0; Indels
                                                                                                                                                                 Indels
           1275 AA; 148879 MW; F006F74BBBB72B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                  73.4%; Score 125.5; DB 2;
42.6%; Pred. No. 2.8e-08;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                   3 TGAPRFIKEV------
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Pfam; PF00078; RVT; 1.
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                                                                                                                     Local Similarity 42,6
les 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DIYRTLHP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIYRTLHP 186
                                                                                                                                                                                                                                                                                                                                                                                 26 DIYRTLHP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYRTLHP 33
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 29; Conserv
           SEQUENCE
                                                                                  Query Match
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DB 2; Length 314;

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119 TGAPREIKQVLSDVQRDLDSHTLIMGDFNTPLSTLDRSTRQKVNKHTQBFNSALHQADLI 178
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  314 AA; 36311 MW; 2C37DD7DD1001A56 CRC64;
                                                    69.3%; Score 118.5; DB Z
39.7%; Pred. No. 5.7e-08;
iive 3; Mismatches 1
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Pfam; PF00078; RVT; 1.
                                                 Query Match
Best Local Similarity 39.77
Matches 27, Conservative
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179 DIYKTLHP 186
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DE HYPOT
OC EUKAT
OC MAMMA
OC MAMMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Tongue;
Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanal H., Watanabe S., Ishida S., Ono Y., Hotura T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamanoto J., Isono Y., Kawai-Hio Y., Salto K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagarama M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AKI31275, BADI8452.1; -
InterPro; IRPR005135; Exo_endo_phos.
Pfamr, PP03372; co_endo_phos; 1.
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Kanehori K., Ishlashi T., Chiba Y., Fujimori K., Hiraoka S.,
Kanehori K., Ishlashi T., Chiba S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamateu A., Ishli S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakahi B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
NnBO human cDNA sequencing project.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AA; 36311 MW; 2C37DD7DD1001A56 CRC64;
                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16220.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ1620 fis, clone CTONG3002552. (Fragment).
Homo sapiens (Human).
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                                              179 DIYRTLHP 186
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DIYKTLHP 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P., Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P., DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.; Mary human Ll alements are capable of retrotransposition.", Nat. Genet. 16:37-43(1997).

EMBL, U93565; AAC51264.1; -.

EMBL, U93565; AAC51264.1; -.

EMBL, W33690; S23690.

O. GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0006278; F:RNA-directed DNA replication; IEA.

InterPro; IPR006135; Exo endo_phos.

InterPro; IPR000477; RVTSe.
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                                                                                                                                                                                        nico sapitens, chumun).
Eukaryota; Macazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-directed DNA polymerase, Transferase.
SEQUENCE 1275 AA; 149007 MW; A866976EA3FD8F74 CRC64;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16190.
Homo sapiens (Human)
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TISSUE-Thalamus;

Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,

Ninomiya K., Wagatsuma M., Kikawa E., Omura Y., Abe K., Kamihara K.,

Ratsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,

A Cusuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

A Kawai-Hio Y., Satio K., Nishikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,

Kanehori K., Takahashi-Fujii A., Oshima A., Kugiyama A., Kawakami B.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

BMBL, AK131258; BAD18436.1:

THERPYO, IPROGNISI; Exo_endo_phos.

R Pfam; PF03372; Exo_endo_phos.

SEQUENCE 202 AA, 22817 MW; B0584E72DF237584 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.3%; Pred. No. 4.9e-08;
Matches 27; Conservative 3; Mismatches 0; Indels 37; Gaps
SEQUENCE FROM N.A.
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4 GAPRFIKEV------QELNSALHQSDLID 26 ò DP DP 8

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27 IXRTLHP 33

180 İYRTLHP 186

Search completed: November 10, 2004, 12:27:09 Job time : 37.1065 secs

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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 19; Conserv
US-09-538-092-914
 FEATURE
 Sequence 914, App Sequence 1315, App Sequence 1305, App Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1148, App Sequence 148, App Sequence 149, App Sequence 16, Appli Sequence 63, Appli Sequence 4263, Appli Sequence 4263, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli
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Copyright (c) 1993 - 2004 Compugen Ltd.
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28 43 44.8 478 3 US-09-274-570-1 Sequence 1, Appli 29 43 44.8 478 4 US-09-440-936-4 Sequence 4, Appli 31 44.8 478 4 US-09-440-936-4 Sequence 830, Appli 32 44.8 577 3 US-09-38-092-830 Sequence 32, Appli 32 44.8 577 3 US-09-389-341-32 Sequence 32, Appli 34 43.8 577 4 US-09-588-092-369 Sequence 369, Appli 35 44.3 822 4 US-09-278-995 Sequence 58656, Appli 42.5 43.8 123 4 US-09-107-5324-4652 Sequence 62321, Appli 36 42 43.8 123 4 US-09-270-767-62321 Sequence 62321, Appli 42 43.8 281 4 US-09-270-767-62321 Sequence 62321, Appli 42 43.8 336 4 US-09-488-25859 Sequence 62321, Appli 42 43.8 573 4 US-09-278-978-5659 Sequence 62321, Appli 42 43.8 573 4 US-09-278-978-5659 Sequence 62321, Appli 42 43.8 573 4 US-09-278-978-5659 Sequence 46706, Appli 42 43.8 573 4 US-09-278-978-5056 Sequence 46706, Appli 42 43.8 503 6 5240706-1 Sequence 470706, Appli 42 43.8 503 6 5240706-1 Sequence 4, Appli 5640706-1 Sequence 4, Appli
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ALIGNMENTS

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| Sequence 4, Application US/08416603
| Patent No. 5866780
| GENERAL INFORMATION:
| APPLICANT: Leaw, Marcus
| APPLICANT: Reddick, Bradford B.
| APPLICANT: Reddick, Bradford B.
| TITLE OF INVENTION: Was Therefor
| TITLE OF INVENTION: Uses Therefor
| NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Saliwanchik & Saliwanchik STREET: Z421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 3266

COMPUTER READABLE FORM:

MEDIUM TYPE: Floopy disk

COMPUTER: BY EC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/416,603

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08987691A
Patent No. 6306387
GENERAL INFORMATION:
APTLICANT: Galan, Jorge E
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEB: Braman & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match

50.0%; Score 48; DB 2; 1

Best Local Similarity 55.0%; Pred. No. 3.7e+02;

Matches 11; Conservative 4; Mismatches 3.
  7; Mismatches
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                                                                   2 NELTRAVEELHKLLKEARE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIOAU JEffrey
REGISTRATION NUMBER: 35,589
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
ENGTH: 3457 amino acids
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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US-08-987-691A-4
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US-08-416-603-4
    Matches
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-108
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT PILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SSCTWARE: Patentin Ver. 2.1
SSCTWARE: Patentin Ver. 2.1
LENGTH: 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: amino acid sequence
US-09-710-279-1302
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SO.0%; Score 48; DB 4; Length 489;
Best Local Similarity 42.1%; Pred. No. 60;
Matches 8; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 512;
                                                                                                                                                                            Length 138;
                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
62;
                                                                                                                                                                         Score 48; DB 3;
Pred. No. 18;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4349, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                          US-09-710-279-1302
; Sequence 1302, Application US/09710279
; Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-4349
                                                                                   TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 DKVKKAADELHKLOKEGKD 412
                                                                                                                                                                                                                                                               1 SNELTRAVEELHKLLKEARE 20
                                                                                                                                                                                                                                                                                             75 NNEVVKLSEENHKLKKELEE 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
42.1%;
                                                                                                                                                                         Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative
      PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3167
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Gaps

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US-09-489-039A-7887
US-09-489-039A-7887
US-09-489-039A-7887
Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIARE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONIARE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONIARE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7887
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1148, Application US/09538092

Patent No. 675334

GENERAL INFORMATION:

APPLICANT: Glot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TILLE PEPERENCE: 15966-542

CURRENT APPLICATION NUMBER: 00/0-03-29

PRIOR FILING DATE: 1090-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1090-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

LENGTH: 787
                                                                                                                                                                                   Score 47; DB 3; Length 563; Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.9%; Score 46; DB 4; Length 508; Best Local Similarity 45.0%; Pred. No. 1.18+02; Matches 9; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.0%; Score 47; DB 4; Length 787; 50.0%; Pred. No. 1.3e+02; Live 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: misc feature

LOCATION: (0)...(0)

OTHER INFOATION: Polypeptide Accession Number P49321
US-09-538-092-1148
                                                                                                                                                                                                                                                     Mismatches
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263 THELTQAVKKIHVIAKELK 281
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                                                                                                                                                                               Ouery Match
Best Local Similarity 42.1%; Pre
Matches 8; Conservative 8;
                                                                                                                                                                                                                                                                                                                 1 SNELTRAVEELHKLLKEAR 19
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7887
                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 10; Conservative
                                                 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-987-691A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-538-092-1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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87;
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; Sequence 2, Application US/08987691A
; Patent No. 6306387
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Galan, Jorge E
TITLE OF INVENTION: ANTIGEN DELIVERY SYSTEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Braman & Rogalskyj, LLP
STREET: P.O. BOX 352
CITY: Canandaigua
STREET: P.O. BOX 352
CITY: Canandaigua
STREET: P.O. BOX 352
COUNTRY: USA
ZIP: 14424-0352
COMPUTER: IEM PC COMPATIBLE
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/987,691A
FILING DATE: 09-NOV-1997
CLASSIFICATION NUMBER: US 60/047,955
FILING DATE: 29-MAY-1997
ATTORNEY/AGBNT INPORMATION:
NAME: Braman, SUSAN I
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,691A
FILING DATE: 09-NOV-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 60/047,955
FILING DATE: 29-MAY-1997
ATTONEY/AGENT INPORMATION:
NAME: Branan, Susan J
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION FOREATION:
TELEFRAM: 716-393-3001
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TELEFRAM: 716-
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REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 001.00151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNELTRAVEELHKLLKEAR 19
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 563 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-691A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-08-987-691A-2
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILL).

TITLE OF INVENTION: UDAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION WHERE: US/99/543,681A

CURRENT PILING DATE: 2000-04-05

PRIOR RILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 599

LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09468253B
Sequence 16, Application US/09468253B
Patent No. 6750012
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Identifying a Psychotropic Agent Using TITLE OF INVENTION: Differential Gene Expression
FILE REPERBNCE: 15966-519
CURRENT APPLICATION NUMBER: US/09/468,253B
GURRENT FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-21
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR RILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21438
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 45; DB-4; Length 252; 56.2%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 4;
Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-543-681A-7699
; Sequence 7699, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NELTRAVEELHKLIKEAR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||||::|::|||
236 LAPAVEEMKRLMREAR 251
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7699
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
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ORGANISM: Homo sapiens
US-09-468-253B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserva
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US-09-468-253B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                                                                                                                                                                                                                                                                                            Sequence 6367, 3pplication US/09107532A
Sequence 6367, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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Pred. No. 44;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSES
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

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NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...131

SEQUENCE DESCRIPTION: SEQ ID NO: 6367:
US-09-107-532A-6367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-252-991A-21438
; Sequence 21438, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 131 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: probLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
TELEPRA: (781)893-527
INFORMATION FOR SEQ ID NO: 6367:
SEQUENCE CHARACTERISTICS:
                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
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66.7%;
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Best Local Similarity 66.7
Matches 10; Conservative
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                                                                                                                                                                                                                                                                              US-09-107-532A-6367
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US-09-468-25B-14

i Sequence 14, Application US/09468253B

Sequence 14, Application US/09468253B

Patent No. 6750012

GENERAL INFORMATION:
APPLICANT GOUID-ROCHDERG, Bonnie
TITLE OF INVENITON: Method of Identifying a Psychotropic Agent Using
TITLE OF INVENITON: Differential Gene Expression
TITLE OF INVENITON: Differential Gene Expression
FILE REFERENCE: 1596-12-20

CURRENT APPLICATION NUMBER: US/09/468,253B

CURRENT APPLICATION NUMBER: 60/113,127

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

TANDE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: D
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US-10-164-595-69
US-10-164-595-69
Sequence 69, Application US/10164595
Patent No. 6657054
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REPERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOCTHANAR: Patentin version 3.1
SEQ ID NO 69
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Query Match
46.9%; Score 45; DB 4; Length 325;
Best Local Similarity 61.1%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 5; Indels
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167 KLKRAVEEVKKLLVPAAE 184
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167 KLKRAVEEVKKLLVPAAE 184
                                                                                                                                                                                         3 ELTRAVEELHKLLKEARE 20
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ORGANISM: Homo sapiens
US-09-468-2538-14
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ORGANISM: Homo sapiens
US-10-164-595-69
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Job time : 6.95679 secs

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Sequence 170935, Sequence 135858, Sequence 135852, Sequence 135990, Sequence 13596, Sequence 135946, Sequence 135946, Sequence 135946, Sequence 135946, Sequence 135946, Sequence 135946, Sequence 12007, A Sequence 12007, A Sequence 12007, A Sequence 12507, A Sequence 12507, A Sequence 125, App Sequence 155, App Sequence 155, App Sequence 155, App Sequence 155, App Sequence 1528, App Sequence 162, App Sequence 162, App Sequence 157958, Sequence 157958, Sequence 1528, App Sequence 162, App Sequence 162, App Sequence 162, App Sequence 162, App Sequence 162, App Sequence 157958, Sequence 25252, App Sequence 25252, App Sequence 25252, App Sequence 162, App Sequence 157958, Sequence 25252, App Sequence 152, App Sequence 152, App Sequence 152, App Sequence 13, Appl

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Length 20;
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US-10-092-750-15

i Sequence 15, Application US/10092750

j Publication No. US20030032157A1

j GENERAL INFORMATION:
   APPLICANT: Harmond, Philip W.
   APPLICANT: Harmond, Philip W.
   APPLICANT: Alphi, Julia
   APPLICANT: Wright, Martin C.
   TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
   TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
   FILE REPERENCE: 50036/050002
   CURRENT APPLICATION NUMBER: US/10/092,750
   CURRENT PLILING DATE: 2002-03-07
   PRIOR FILING DATE: 2001-03-08
   NUMBER OF SEQ ID NOS: 253
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 15
   LENGTH: 20
   TENGTH: 20
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5 US-10-437-963-170935

5 US-10-437-963-13958

6 US-10-437-963-135898

6 US-10-437-963-135898

6 US-10-437-963-135898

6 US-10-437-963-135990

6 US-10-437-963-135996

6 US-10-437-963-135985

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6 US-10-437-963-135995

6 US-10-282-122A-70340

US-09-815-242-12607

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-092-750-244
is Sequence 244, Application US/10092750
i Publication No. US20030032157A1
i GENERAL INFORMATION:
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Sequence 244, App
Sequence 166019,
Sequence 160411,
Sequence 160467,
Sequence 18518, Ap
Sequence 135978,
Sequence 135978,
Sequence 160433,
Sequence 160433,
Sequence 160478,
                                                                                                                                                           November 10, 2004, 15:53:52; Search time 19.2901 Seconds (without alignments) 366.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/PcT_RWW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PcT_RWW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PcT_RWW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_RWW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_RWW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_RWW PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-092-750-244
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US-10-437-96-116315019
US-10-424-599-160411
US-10-424-599-160467
US-10-424-599-160467
US-10-424-599-160467
US-10-437-96-135978
US-10-437-96-135978
US-10-437-96-135978
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                                                                                                                                                                                                                                                                                                                                                                                                                    1566620 segs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                     1 SNELTRAVEELHKLLKEARE 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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96
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Result No.

9224084684824

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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Phil
TITLE DE INVENTION: Rice Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53221)B
CURRENT APPLICATION WINGER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 163252
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 160411, Application US/10424599
Sequence 160411, Application No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yahua
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: La Cao Yongwei
APPLICANT: APPLICANT: January Say Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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53.1%; Score 51; DB 16; Length 418;
Best Local Similarity 58.8%; Pred. No. 60;
Matches 10; Conservative 3; Mismatches 4; Indels
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US-10-424-599-160411
                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: PAT_MRT4530_62266C.1.pep
US-10-437-963-163252
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LOCATION: (1)..(329)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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72 AKEYEKAIEELQKLLREKSE
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oryza sativa FEATURE:
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US-10-424-599-160467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.7%; Score 89; DB 14; Length 122; Best Local Similarity 95.0%; Pred. No. 8.2e-05; Matches 19; Conservative 0; Mismatches 1; Indels
   APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Uulia
APPLICANT: Alpin, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 244
LENGTH: 122
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US-10-437-963-136019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 SNELTRAVEELHKLLKEAGE 50
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-244
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US-10-437-963-163252
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Sequence 135978, Application US/10437963 .

Sequence 135978, Application US/10437963 .

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

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APPLICANT: Boukharov, Andrey A.

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Sequence 135893.

Sequence 135893.

Publication No. US20040123343A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 2016/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 133893

LENGTH: 328
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                                                                                                                                                                                                                                                                        Score 49; DB 17; Length 294;
Pred, No. 79;
4; Mismatches 6; Indels
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US-10-437-963-135978
                                                                                                                                                         ) OTHER INFORMATION: Clone ID: GLYMA-23APR03-C1728_56.p
US-10-739-930-8785
    NAME/KEY: unsure
LOCATION: (1)..(294)
OOTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SNELTRAVEELHKLLKEARE 20
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Best Local Similarity 50.0%;
Matches 10; Conservative
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Sequence 186169, Application US/10424599
Publicanton No. US20040031072A1
Sequence 186169, Application No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS REPRESENCE: 38-21 (5223.3) B
CURRENT APPLICANT: 2003-04-28
NUMBER OF SEQ ID NOWER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 87
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US-10-739-930-8785

Sequence 8785, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: KOVA16.
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

CURRENT APPLICATION ON UNMER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 8785

LENGTH: 294
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52.1%; Score 50; DB 15; Length 339;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 10; Conservative 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure

LOCATION: (1)..(339)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_11591C.1.pep
US-10-424-599-160467
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 160467
LENGTH: 339
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Best Local Similarity 50.0%
Best Local 10, Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
FEATURE:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Sic Pulant Sic Pulant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 170935
LENGTH: 392
                                                                                                                                                           Sequence 257223, Application US/10424599
| Sequence 257223, Application US/10424599
| Publication Wo. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua |
| APPLICANT: Zhou Yihua |
| APPLICANT: Cao Yongwei |
| TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement |
| TITLE OF INVENTION: 2003-04-28 |
| CURRENT FILING DATE: 2003-04-28 |
| SEQ ID NO 25723 |
| LENGTH: 345 |
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US-10-424-599-257223
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US-10-437-963-170935
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72 AKEYEQAIEELQKLLREKSE 91
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                        1 SNELTRAVEELHKLLKEARE
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ORGANISM: Oryza sativa
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ORGANISM: Glycine max
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
APPLICANT:
Cao Yongwei
TITLE OF INVENITON:
FILE PEPERRONE: 38-21(5323)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 160433
LENGTH: 330
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Bublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cov Vanic David K
APPLICANT: Cov Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 160478
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                                                                                                                                              Query Match 51.0%; Score 49; DB 16; Length 328; Best Local Similarity 52.6%; Pred. No. 86; Matches 10; Conservative 2; Mismatches 7; Indels
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                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_37524C.1.pep
US-10-437-963-135893
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US-10-424-599-160433
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US-10-424-599-160478
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                                                                                                                                                                                                                                                        2 NELTRAVEELHKLLKEARE 20
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Best Local Similarity 50.0%
Matches 10, Conservative
TYPE: PRT ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
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us-10-092-750-15.rapb
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RESULT 15

US-10-437-963-135858

US-10-437-963-135858

Sequence 135858, Application US/10437963

Sequence 135858, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: Rice Nucleic Acid Molecules

TITLE OF STORING PATE: 2003-05-14

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 135858

LENTH: 483

LENTH: 483
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Best Local Similarity 52.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 2; Mismatches 7; Indels
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ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(483)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
CHER INFORMATION: Clone ID: PAT_MRT4530_37493C.1.pep
US-10-437-963-135858
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 4.04321 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-15 96 1 SNELTRAVEELHKLLKEARE 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	tpr protein - huma	UDPgalacturonate d	ATP synthase, B ch	assemblin, striate	hypothetical prote	ed hyp	capsid protein [ba	phosphoketolase (i	hypothetical prote	hypothetical prote	tyrosine phosphata	nuclear autoantige	transcription regu	SYR1-like syntaxin	sensor protein Pho	sensor kinase phoQ	sensor protein Pho	L-aspartate oxidas	nuclear autoantige	gene 22 protein -	ribosomal protein	30S ribosomal prot	mal pro	type 4 fimbrial bi	deoxyribose-phosph	GRESAG protein 2.1	hypothetical prote	translation releas	L-seryl-tRNASec se
SOPPRATES		S33124	S29787	C82716	A40689	E71169	F89922	AC1754	F86812	T00415	T25368	AB0850	A48819	D69749	C85042	G85686	B41966	A99829	T36393	A43800	WZBE22	R3HS9H	H84321	R3HS19	8307	8287	B39685	1513	4808	8603
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L-seryl-tRNASec se	_	sensor kinase phoQ	sensor protein Pho		hypothetical prote			-н		purine NTPase [imp	hypothetical prote	transcription regu	carbonate dehydrat	CD	thiosulfate sulfur
	A651	VZEBPT	AG0646	T19281						ш		ď		æ	B7045
63	463 2		87	677 2	885 2	961 2				864 2	겁	51	9	81	93
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			45		45	45	45	45	45	44.5	44	44	44	44	44
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		RESULT 1 \$33124
	٠.	tpr protein - human . NyAltarnate names: kinase-related transforming protein (tpr-met); protein with promoter 1 . Organise: Home easiens (man)
		Nintcoment, 2309-2313, Looper, C.S. Oncogene 7, 2309-2313, 1992 A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coil
		A; Status: preliminary; nucleic acid sequence not A; Molegule type: mRNA
. *[:		A;Kesiques: 1-2094 cMil. A;Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; EMBL:X66397; NID:g633225 ». Moro: the minisoride commence was submitted to the EMBT. Data filtrary. Orthher 1991
		A;Note: the nucleotine sequence was submitteed to the brain Date brains; occopies 15:3:3:3:3:3:3:3:3:3:3:3:3:3:3:3:3:3:3:3
		Oncogene 7, 383-388, 1992 A;Tile: Nucleotide sequence analysis of human tpr cDNA clones.
4.		A; Metricine number: 023/10; Morb.321530/0; Filt.1315333 A; Accession: S23740
١.		A;Status: preliminary
		A;Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258 R:xing H W.S. Tempest, P R.: Marrifield, K.R.: Rance, A.J.
		A.A.M., named 2, 617-619, 1988
		AjTitle: Tpr homologues activate met and raf. BiBefarence mumher: S00928: MITD:88262257: PMTD:3387099
		A.Acceston: 800928
		A; Molecule type: mRNA
		A;Cross-references: EMBL:V00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
		R;Greco, A. submitted to the EMBL Data Library, December 1995
		A; Reference number: H00592
		A, Status: translated from GB/EMBL/DDBJ
		A,Molecule type: DNA a.residins: 144.228 (GRE.
		A; Cross-references: EMBL: X94208; NID: g1296797; PIDN: CAA63904.1; PID: g1296798
		C;Genetics: A:Gene: GDB:TDR
		A;Cross-references: GDB:128821; OMIM:189940 A;Map position: 1q25-1q25
		A;Introns: 177/3
		Query Match 92.7%; Score 89; DB 2; Length 2094; Best Local Similarity 95.0%; Pred. No. 0.00081; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A.Jatuthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: H+-transporting ATP synthase chain I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assemblin, striated fiber - green alga (Spermatozopsis similis)
NyAlternate names: beta-giardin homolog SF-assemblin; striated microtubule associated systemate names: beta-giardin homolog SF-assemblin; striated microtubule associated systemate 2.5pecies: Spermatozopsis similis
C;Species: Spermatozopsis similis
C;Accession: A40689; S29746
R;Weber, K.; Geisler, N.; Plessmann, U.; Bremerich, A.; Lechtreck, K.F.; Melkonian, M.
J. Cell Biol. 121, 837-845, 1993
A;Title: SF-assemblin, the structural protein of the 2-nm filaments from striated microtic A;Accession: A40689; MUID:93260016; PMID:8491776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71169
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekink R;Kawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic and A;Reference number: A71000; WUID:98344137; PMID:9679194
A;Accession: E71169
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A,Note: this accession replaces an interim accession for a sequence replaced by GenBank C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.1%; Score 50; DB 2; Length 156; Best Local Similarity 61.1%; Pred. No. 11; Matches 11; Conservative 2; Mismatches 5; Indels
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Best Local Similarity 47.1.
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Matches 9, Conserv
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A;Residues: 1-399 <KAW>
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A,Molecule type: DNA
A,Moresi 1-587 <BEN>
A,Cross-references: UNIPROT:Q06700, EMBL:X69435, NID:g49181, PIDN:CAA49210.1, PID:g49182
A,Accession: S61762
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C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Accession: C82716
A;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 2000
A;Title: The genome Sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Accession: C82716
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Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marfino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Bendrat, K.; Buckel, W.

Bur. J. Biochem. 211, 697-702, 1993
A/Title: Cloning, sequencing and expression of the gene encoding the carboxytransferase erichia coli.
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A,Reaidues: 'X',3-22,'X',24-35,454-461 <BEW>
R;Bendrat, K.; Mueller, U.; Klees, A.G.; Buckel, W.
FEBS Lett. 329, 329-331, 1993
A;Title: Identification of the gene encoding the activator of (R)-2-hydroxyglutaryl-CoA,
A;Reference number: S36104, MUID:93374040; PMID:8365476
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C;Keywords: carbon-carbon lyase; carboxy-lyase
F;2-587/Product: UDPgalacturonate decarboxylase alpha chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                        UDPgalacturonate decarboxylase (EC 4.1.1.67) alpha chain - Acidaminococcus fermentans N;Alternate names: UDPgalacturonate decarboxylase carboxytransferase chain C;Specias: Acidaminococcus fermentans C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: S29787; S61762; S36104; S28382
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A;Residues: 548-587 <BE2>
A;Cross-references: EMBL:X59645; NID:g433930; PIDN:CAA42195.1; PID:g433931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;Reference number: $29787; MUID:93170302; PMID:8382157
                                                                                                 SNELTRAVEELHKLIKEAGE 319
                       SNELTRAVEELHKLLKEARE 20
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nes 9, Conserv
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hypothetical protein Y57G11B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cact-1999 #text_change 09-Jul-2004
C;Accession: T25368, T27214
R;Cummings, P.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z20023
A;Reference number: Z20023
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-418 < WIL>
A;Residues: UNIPROT: C18223; EMBL: Z82284; PIDN: CAB05295.1; GSPDB:GN00022; CESP: Y5'
A;Resperimental source: Clone T27E7
A;Reference number: Z20329
A;Accession: T27214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T27214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-418 < WIL>
A;Residues: 1-418 < WIL>
A;Residues: L418 < WIL>
A;Residues: L418 < WIL>
A;Residues: Caenores: EMBL: Z99280; PIDN: CAB16502.1; GSPDB:GN00022; CESP: Y57G11B.1
A;Experimental source: clone Y57G11B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein H_248015.1 - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00415
R;Fhlton, B:, Nham, M.; Hawkins, J.; Beck, C.
R;Fhlton, B.; Nham, M.; Hawkins, J.; Beck, C.
R;Fhlton, B.; Nham, M.; Hawkins, J.; Beck, C.
A;Beference number: 214148
A;Accession: T00415
A;Accession: T00415
A;Accession: T00415
A;Accession: T00415
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 1-1849 <FUL>
A;Residues: 1-1849 <FUL>
A;Accession: T00415
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A;Accession: T00415
A;Accession: T00415
A;Accession: T00415
A,Title: The complete genome sequence of the lactic acid bacterium Lactoccocus lactis sspanseerence number: A86625; MUD:21235186; PMID:11337471
A,Rocusion: F86812
A,Status: preliminary
A;Molecule type: DNA
A,Rosidues: 1-822 - SSTO-
A,Forsel-references: UNTPROT:09CFH4; GB:AE005176; PID:g12724499; PIDN:AAX05600.1; GSPDB:GR
A,Experimental source: strain IL1403
C,Genetics:
A,Genetics:
C,Superfamily: phosphoketolase
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Pred. No. 2.3e+02;
1; Mismatches 2; Indels
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76.9%;
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259 KAIEDIHQIQKDARE 273
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407 VEELHPLMKEALE 419
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Best Local Similarity 76.9
Matches 10; Conservative
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A;Note: H_248015.1
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AC1754
Capsid protein [bacteriophage bIL285] homolog lin2576 [imported] - Listeria innocua (str
C'Species: Listeria innocua
C'Species: Listeria innocua
C'Species: Listeria innocua
C'Species: Listeria innocua
C'Species: Listeria innocua
C'Species: Listeria innocua
C'Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C'Accession: AC1754
R'Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C'Accession: AC1754
R'Glaser, D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, B.
Science 294, 849-852, 2001
A,Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession: AC1754
A,Status: preliminary
A,Residues: 1-395 AGLA>
A,Cross-references: UNIPROT:0928F9; GB:AL592022; PIDN:CAC97803.1; PID:gl6415098; GSPDB:G
A,Genetics:
C,Genetics:
A,Gene: lin2576
                                                                                                                                                                                           conserved hypothetical protein SA1279 [imported] - Staphylococcus aureus (strain N315) c.95ecies: Staphylococcus aureus SA1279 [imported] - Staphylococcus aureus (strain N315) c.95ecies: Staphylococcus aureus arevision 10-May-2001 #text_change 24-Nov-2003 C.96cession: P89922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 R.922 
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86812
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrligenome Res. 11, 731-753, 2001
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K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 48; DB 2; Length 114; llarity 50.0%; Pred. No. 15; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 48; DB 2; Length 395; 52.6%; Pred. No. 50; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SNELTRAVEELHKLLKEARE 20
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71 DELTAKIEELEKELEEAND 89
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Matches 10; Conservative
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es 10; Conserv
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Cispecies: Bacillus subtliss
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence 07-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence 07-Dec-1997 #text_change 09-Jul-2004
A. Ehrlich, S.D.; Bemerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A.; Ehrlich, S.D.; Enger, M.; Fullbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Latuber, J.; Harwood, C.R.; Jodesev, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, N.; Rivitors: Lauber, J.; Jodesev, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sexonon, A.; Aluthors: Schleich, S.; Schreeter, R.; Scoffene, F.; Sekigundi, A.; Jesako, M.; Serono, A.; Hulle, M.; Tamakoshi, A.; Tamaka, T.; Terpstera, P.; Tognoni, A.; Tosato, V.; Voshida, K.; Aluthors: Voshida, M.; Tamakoshi, A.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Yoshida, M.; Alatus: preliminary; nucleic acid sequence of the Gram-postiive bacterium Bacillus subtilis.
A;Rocession D69749 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: C85042
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Rature 402, 769-777, 1999
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:031449; GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12016.1
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q9ZQZ8; GB: NC_001268; NID: g7270203; PIDN: CAB77818.1; GSPDB: GP. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substrain EDL933)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYR1-like syntaxin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensor protein PhoQ [imported] - Escherichia coli (strain 0157:H7, substrai)
C,Species: Escherichia coli
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
- Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
transcription regulator AraC/XylS family homolog ybfI
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Pred. No. 65;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB Pred. No. 72; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NELTRAVEELHKLLKEARE 20
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Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RAVEELHKLIKEARE 20
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51 KAVDEIHKRLQDANE 65
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Best Local Similarity 53.3,
Local Similarity 53.3,
Local Similarity
Local Similarity
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C;Superfamily: syntaxin
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-305 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine phosphatase (associated with virulence) [imported] - Salmonella enterica subsp. C,Species: Salmonella enterica subsp. enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
A,Note: this species has also been called Salmonella typhi
C,Accession: AB0850
B,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, I.T., T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atthors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atthors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; MUD:21534947; PMID:11677608
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A;Status: preliminary
A;Mosicule type: nucleic acid
A;Rosicule type: 1787 cOIR>
A;Cross_references: UNIPROT:P49321; GB:M97856; NID:G184432; PIDN:AAA36027.1; PID:G184433
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A;Residues: 1-543 <PAR>
A;Crossidues: 1-543 <PAR>
A;Crossidues: GB:AL513382; PIDN:CAD05985.1; PID:g16503956; GSPDB:GN00176
C;Genetics:
A;Gene: stpA
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C;Species: Homo sapiens (man)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                              4.
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                                                                                                                        49.0%; Score 47; DB 2; Length 418; 56.5%; Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2; Length 543; Pred. No. 93; 8; Mismatches 3; Indels
                                                                                                                                                                                           5; Indels
A;Gene: CESP:X57G11B.1
A;Map position: 4
A;Introns: 33/3; 63/1; 94/2; 143/3; 228/2; 285/3; 340/3
                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                       2 NELTRAVEELH----KLLKEARE 20
                                                                                                                                                                                                                                                                                                     NELKRRNDEAHSQYMKELKEARE 65
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                                                                                                                    Query Match
Best Local Similarity 56.5'
Matches 13; Conservative
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Best Local Similarity 42.1<sup>3</sup>
Matches 8; Conservative
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Best Local Similarity
Matches 10; Conserv
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RESULT 13

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C; Accession: G85686

R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhex iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Residues: Draliminary

A; Molecule type: DNA

A; Residues: 1-460 <STO>
A; Cross-references: UNIPROT:Q8X739; GB:AE005174; NID:g12514780; PIDN:AAG55955.1; GSPDB:G
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: phoQ
C; Superfamily: envZ protein; sensor histidine kinase homology
Query Match
A7.9%; Score 46; DB 2; Length 460;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
C)
Db 218 TRELTSLVRAINRLEKSERE 237
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Search completed: November 10, 2004, 12:29:19 Job time : 5.04321 secs

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Q8rgd8 fusobacteri Q877h8 sulfolobus Q8561 enterobacte Q928f9 listeria in Q73b78 bacillus ce Q81f51 bacillus an Aas40471 bacillus Aat30537 bacillus

Q7qtr3 giardia lam Q84sq3 oryza sativ Q8cmkl staphylococ

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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=93064711; PubMed=1437155; Mitchell P.U., Cooper C.S.; Mitchell P.U., Cooper C.S.; The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Tpr protein.
Name-Tpr;
Name-Tpr;
Name-Tpr;
Mammalia, Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 92.7%; Score 89; DB 2; Length 726; Similarity 95.0%; Pred, No. 0.0033; 19; Conservative 0; Mismatches 1; Indels
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Nucleoprotein TPR.
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AAS40471
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Q7QTR3
Q84SQ3
                      Q877H8
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Q73B78
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Q73z23 mycobacteri
Q73z23 mycobacteri
Q64yF9 oryza sativ
Q6700 acidaminoco
Q9pe81 xylella fas
Q7uw14 rhodopirell
Q81z81 methanopyru
P55925 spermatozop
Q5288 pyrococcus
Q7xx19 oryza sativ
Q75x15 oryza sativ
Q75x170 oryza sativ
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Q7a0v6 staphylococ
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Q6g9b7 staphylococ
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Q6G9B7
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Gapop 10.0 , Gapext 0.5
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Result õ ö

Gaps

PRT; 2363 AA

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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                      Name=tpr;
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DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its modified an on-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.;

"top homologues activate met and raf.";

"top homologues activate met and raf.";

"noncogene 2:617-619(1988).

"FUNCTION: Component of the cytoplasmic fibrils of the nuclear pore complex implicated in nuclear protein import. Its amino terminus is involved in activation of oncogenic kinases.

"SUBCELLUIAR LOCATION: Cytoplasmic surface of the nuclear pore complex. The assembly of the NPC is a stepwise process in which Trp-containing peripheral structures assemble after other components, including p62.

"Trp-containing peripheral structures assemble after other components, including p62.

"Trp-containing peripheral structures assemble after other components, including p62.

"Trp-containing peripheral structures assemble after other brain, lower levels in heart, liver and kidney.

"Trp-containing the peripheral structure and kidney.

"Trp-containing peripheral structure and kidney.

"Trp-containing peripheral structure and kidney.

"Trp-containing peripheral structure and kidney.
                 Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinase, is localized to the cytoplasmic surface of the nuclear pore complex."; J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 1; Length 2349;
Pred. No. 0.0095;
); Mismatches 1; Indels
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EMBL; Y00672; CAA68681.1; -.
Genew; HGNC:12017; TPR.
MIM; 189940; C:Cytoplasm; TAS.
GO; GO:0005737; C:Cytoplasm; TAS.
GO; GO:0005643; C:nuclear pore; TAS.
GO; GO:0005669; P:protein-uncleus import; TAS.
Chromosomal translocation; Coiled coil; Nuclear protein;
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SEQUENCE OF 1-142 FROM N.A.
MEDLINE=68262257; PubMed=3387099;
  MEDLINE=95096166; PubMed=7798308;
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MEDLINE=97177132; PubMed=9024684;
Cordes V.C., Raidenbach S., Rackwitz H.R., Franke W.W.;
Cordes V.C., Patdenbach S., Rackwitz H.R., Franke W.W.;
"Identification of protein p270/Thras as constitutive component of the
nuclear pore complex-attached intranuclear filaments.";
J. Cell Biol. 136:515-529(1997).
EMBL; U69668; AAB48030.1; -. SEQUENCE 2363 AA; 267333 WW; E9BAIC6E78AA35B0 CRC64;
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STRANTESTBL/GJ TISSUE=Whole body;
The FANTOM COMSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECTION N.A.
STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NMR-2003 (TrEMBLrel. 23, Created).
01-NMR-2003 (TrEMBLrel. 23, Last sequence update)
01-UMN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610029M07 product:NUCLEAR PORE COMPLEX-
ASSOCIATED PROTEIN TPR homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2363;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

92.7%; Score 89; DB 2; Length 236
Best Local Similarity 95.0%; Pred. No. 0.0095;
Matches 19; Conservative 0; Mismatches 1; Indels
                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  Created)
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STRAIN-C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
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01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-OCT-2002 (TrEMBLrel. 22,
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Gaps

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300 SNELTRAVEELHKLLKEAGE 319

RESULT 3 Q99968

1 SNELTRAVEELHKLLKEARE 20

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STRAIN=NOD; TISSUE=Thymus;

A Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Haraka T., Hirozane T.,

A Hayashida K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,

A Hori F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Myazaki A., Murata M., Nakamura M.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Sasito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Basaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Charu A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

EMBL, AKO88078, BAG40132.1;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALTH-NOD, TIESUE=Thymus;
MEDLINE=2049374; PubMed=11042159;
MEDLINE=2049374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SITAIN=NOD; TISSUE=Thymus;

C STRAIN=NOD; TISSUE=Thymus;

MEDILINE=200313; PubMed=11076861;

A MEDILINE=200313; PubMed=11076861;

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Namamoto R., Nakamura S., Hazama M., Nishine T., Harada A.,

A Vamamoto R., Inoue K., Toakaguchi S., Ikegami T., Kashiwagi K.,

A Pujiwake S., Inoue K., Toawaw Y., Izawa M., Ohara E., Watshiki M.,

A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,

TRIEN integrated sequence analysis (Rish) system-384 format

Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                          SEQUENCE FROM N.A. STRUMLS; STRUMLS, STRUMLS, TISSUE-THYMUS; STRANDW CORSOLTIUM, TEANTOW CORSOLTIUM, THE FANTOW CORSOLTIUM, The FANTOW CORSOLTIUM, THE RIKEN GENOME Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation (6.0, 770 full)-length cDNAs."; Nature 420:563-573 (2002).
             RIKEN FANTOM COnsortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Last sequence update)
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GO; GO:0005635; C:nuclear membrane; IDA.
MEDLINE=21085660; PubMed=11217851;
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(TrEMBLrel. 24, I
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nes 18; Conservative
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ID Q9211
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A Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,

A Adachi J., Alzawa K., Akahira S., Rukunishi Y., Furuno M.,

RA Arakawa T., Bonoo H., Carminci P., Furuno C., Hiraoka T., Hori F.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Matsuyama T., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakio C., Sakai K.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., S.,

RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,

B. Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR MGD; MGI.1922066; TDr.,

DR MGD; MGI.1922066; TDr.,

DR GO; CO:0005635; C:nuclear membrane; IDA.
           "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20530913; PubMed=11070661;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nafeunai T., Tashinc H., Itoh M., Sumanoto R., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yuliwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watsahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated Sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:E430003121 product:NUCLEAR PORE
COMPLEX-ASSOCIATED PROTEIN TPR homolog (Fragment).
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Pred. No. 0.0048;
1; Mismatches 1; Indels
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     Okazaki Y., Muramatsu M., Hayashizaki Y.;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN-NOD; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
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STRAIN=NOD; TISSUE=Thymus;
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Best Local Similarity 90...
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BMBL, AABFO100062; EAA24012.1; -.

GO, GO:00164691; C:proton-transporting two-sector ATPase complex; IEA.
GO; GO:0016693: F:hydrogen-transporting ATP synthase activity. .; IEA.
GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0016820; F:hydrogen-transporting ATPase activity, rota. .; IEA.
GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.
GO; GO:0015986; P:hydrolase activity, acting on acid anhydrid. .; IEA.
InterPro; IPR002146; ATPSynthesis coupled proton transport; IEA.
InterPro; IPR005864; ATPSynthFO_B.
Pfam; PF00430; ATP-synt B; 1.
TIGREAMS; TIGGAN144; ATP synthFO_B.
TIGREAMS; TIGGAN144; ATP synthFO_B.
CF(0); Hydrogen ion transport; Hydrolase; Transmembrane.
SEQUENCE 163 AA; 18894 MM; 92AF893E3718C92F CRC64;
                                                                                                                                                                                                                                                                                                                                             H(+) (Out).

-1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1) (By
                                                                                                                                                                                       Karpetral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N., Eastern S., Overbeek R., Syrpides N., Submitted (JAN-2003) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SIMILARITY: Belongs to the ATPase B chain family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/Genbank/DDBJ databases.
-1- SIMILARITY: Belongs to the acyl-CoA dehydrogenase family.
EMBL, AE017232; AAS003775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium,
Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006090; Acyi-CoA dh C.
InterPro; IPR006091; Acyi-CoA dh M.
InterPro; IPR006091; Acyi-CoA dh M.
InterPro; IPR0060905; Acyi-CoA dh M.
InterPro; IPR0090915; Acyi-CoA dh M.
InterPro; IPR009100; AcyICoA dehyd NM.
Pfam; PF00441; Acyi-CoA dh; I.
Pfam; PF00770; Acyi-CoA dh; I.
Pfam; PF00770; Acyi-CoA dh; I.
Complete protecome; FAD; Plavoprotein; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.1%; Score 51; DB 2; Length 163; larity 66.7%; Pred. No. 76; Conservative 2; Mismatches 3; Indels
      Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
EMBL; AABF01000062; EAA24012.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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85 KAEEEAHNLIKEARE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
OrderedLocusNames=MAP1458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 RAVEELHKLIKEARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
ses 10; Conserv
                                                             NCBI_TaxID=209882;
                                                                                                                                                                STRAIN=ATCC 49256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
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Matches
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      A PART OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE OF CARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The evolutionarily conserved single-copy gene for murine Tpr encode one prevalent isoform in somatic cells and lacks paralogs in higher
Mus muscúlus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Nuclear pore complex-associated intranuclear coiled-coil protein
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SEQUENCE FROM N.A.
MEDLINE-22310828; PubMed=12424524;
Kuznetsov N.V., Sandblad L., Hase M.E., Hunziker A., Hergt M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kuznetsov N.V., Sandblad L., Hase M.E., Hunziker A., Hergt M.,
Cordes V.C.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ298076; CAC40701.1; -
MGD; MGI:1922066; Tpr.
GO; GO:0005555; C:nuclear membrane; IDA.
SEQÜENCE 1200 AA; 138973 MW; 616663FBA6B267D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosoma 111:236-255 (2002).
-!- MISCELLANEOUS: The sequence shown here is derived from an BMBL/Genbank/DDBU third party annotation (TPA) entry.
EMBL; BKG00023; DAA00370.1; -.
SEQUENCE 2357 AA; 266924 MW; 3DA5A0FE2457453F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match B9.6%; Score 86; DB 2; Length 1200; Local Similarity 90.0%; Pred. No. 0.013; les 18; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.6%; Score 86; DB 2; Length 2357; 90.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP synthase B chain, sodium ion specific (EC 3.6.3.15).
Name=FNV0984;
Fusobacterium nucleatum subsp. vincentii ATCC 49256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Q7PSL1;
01-MAR-2004 (TEMBLrel. 26, Created)
01-MAR-2004 (TEMBLrel. 26, Last sequence update)
01-MAR-2004 (TEMBLrel. 26, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eukaryotes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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Q7M739
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Best Local Similarity 58.8°
Matches 10, Conservative
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Q06700;
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GCDA ACIFE
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                                                                               Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Putative Sec14 cytosolic factor (Phosphatidylinositol/phosphatidyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017232; AAS03775.1; -.
Hypothetical protein.
SEQUENCE 392 AA; 43695 WW; 1E7EABECSB045968 CRC64;
                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.1%; Score 51; DB 2; Length 392; Best Local Similarity 52.6%; Pred. No. 1.7e+02; Matches 10; Conservative 4; Mismatches 5; Indels
                                            53.1%; Score 51; DB 2; Length 392; llarity 52.6%; Pred. No. 1.7e+02; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki T., Matsumoto T., Katayose Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005641; BAC57373.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; TPR001251; CRAL TRIO C.
InterPro; IPR008273; CRAL TRIO N.
InterPro; IPR01074; Sec14p_like_N.
Pfam; PF00550; CRAL TRIO; 1.
Pfam; PF03765; CRAL TRIO, 1.
SMART; SM00516; SEC14; 1.
SECUENCE 418 AA; 47494 MW; EDF950C186EC6C98 CRC64;
                   392 AA; 43695 MW; 1E7EA8EC5B045968 CRC64;
                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 AA
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250 AGDLRRAVEELHELARRPR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AGDLRRAVEELHELARRPR 268
                                                                                                          1 SNELTRAVEELHKLLKEAR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNELTRAVEELHKLLKEAR 19
                                                                                                                                                                                                                                                                                                                      Mycobacterium paratuberculosis.
                                                                                                                                                                                                                                      02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         choline transfer protein). Name=OSJNBa0027N13.111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                     Hypothetical protein.
MAP1458.
                                                            Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; Q84YR9;
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1770;
      Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=k10;
                                                                                                                                                                                                             AAS03775
AAS03775;
                   SEQUENCE
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q84YR9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q84YR9
                                                                         Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINES22737481, PubMed=12853465;
MEDLINES.2737481, PubMed=12853465;
Mendt K.S., Schall I., Hüber R., Buckel W., Jacob U.;
"Crystal structure of the carboxyltransferase subunit of the bacterial
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                               Acidaminococcus fermentans.
Bacteria, Firmicutes, Clostridia, Clostridiales, Acidaminococcaceae,
Acidaminococcus.
NCBI_TaxID=905,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Decarboxylase szubunit of the primary sodium pump glutaconyl-CoA decarboxylase (GCD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Anaerobic glutamate metabolism; fifth step.
-!- SUBUNIT: Heteroctamer consisting of two alpha, two beta, two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 548-587 FROM N.A.
STRAINS-ATCC 25085;
MEDLINE-33374040; PubMed-8365476;
Bendrat K., Muallar U., Klees A.-G., Buckel W.;
Bendrat K., Muallar U., Klees A.-G., Buckel W.;
"Identification of the gene encoding the activator of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermentans Gene expression in Bacherichia coli.";
FEBS Lett. 329:329-331(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, sequencing and expression of the gene encoding the carboxytransferase subunit of the biotin-dependent Na+ pump glutaconyl-CoA decarboxylase from Acidaminococcus fermentans in Escherichia coli.";
                                          ö
Score 51; DB 2; Length 418;
Pred. No. 1.8e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 25085;
MEDLINE=95331308; PubMed=7607244;
Mueller U., Buckel W.;
Addivation of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaninococcus fermentans.";
Eur. J. Biochem. 230:698-704(1995).
                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2004 (Rel. 45, Last annotation update)
01-CCT-COA decarboxylase alpha subunit (EC 4.1.1.70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sodium ion pump glutaconyl-coenzyme A decarboxylase.";
EMBO J. 22:3493-3502(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 carboxyltransferase domain.
                                                                                                                                                                                                                587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 211:697-702(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 25085,
MEDLINE-93170302; PubMed-8382157;
Bendrat K., Buckel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma and two delta subunits.
                                          'n
                                                                                                  ||| :|:| |||:||
389 NELANHIEQLRKLLREA 405
                                                                               2 NELTRAVEELHKLLKEA 18
    53.1%;
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                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                (Carboxyltransferase).
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Gaps

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HISSP, P00859; 112P.

GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.

GO; GO:00166913; F:hydrogen-transporting ATP synthase activity.

GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota.

GO; GO:0016820; F:hydrogen-transporting ATPase activity, rota.

GO; GO:0016820; F:hydrogen-transporting ATPase activity, rota.

GO; GO:0016820; F:hydrodase activity, acting on acid anhydrid.

GO; GO:0015986; P:HP synthesis coupled proton transport; IEA.

InterPro; IPR002146; ATPsynt B/B'sub.

InterPro; IPR00306; ATPsynt B/1.

IGREAMS; IIGR01144; ATPsynt B/1.

TIGREAMS; TIGR01144; ATPsynt Lb/1.

CF(0); Complete protecme; Hydrogen ion transport; Transmembrane.

SEQUENCE 156 AA; 17461 MW; 11169746B7ADESAC CRC64;
subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50, DB 2; Length 156;
Pred. No. 99;
2; Mismatches 5; Indels
                           similarity).
-!- SIMILARITY: Belongs to the ATPase B chain family.
EMBL, AE003950; AAF83957.1; -.
HSSP; P00859; 1L2P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.1%; Score 50; 61.1%; Pred. No.
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01-071-201 (TremBlrel. 25, 14)
01-071-201 (TremBlrel. 25, 16)
01-071-201 (TremBlrel. 25, 16)
01-071-201 (TremBlrel. 25, 16)
01-071-201
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Matches 11; Conservative
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ID RPOL METKA
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Q7UWL4;
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Q7UWL4
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                                                                                   BIRDIA; S29787; S29787; S29787; PDR; S29787; S29787; S29787; S29787; S29787; S29787; S29787; S29787; Mibosomal H2TH.

InterPro; IPRO10079; Ribosomal H2TH.

PROSITE; PS50989; COA CT CTER; 1.

PROSITE; PS50980; COA CT CTER; 1.

PROSITE; PS50980; COA CT WIER; 1.

3D-structure; Biotin; Decarboxylase; Direct protein sequencing; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate H(+) (Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
53.1%; Score 51; DB 1; Length 587
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                       535 568 Carboxyltransferase.
587 Aa; 64346 MW; BFICOD2F2DCA86DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20365717; PubMed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ELTRAVEELHKLIKEARE 20
                                        EMBL; X69435; CAA49210.1; -. EMBL; X59645; CAA42195.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonadaceae; Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP synthase, B chain.
OrderedLocusNames=Xf1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                              Sodium transport.
DOMAIN 35
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Q9PE81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                  Bacteria: Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
52.1%; Score 50; DB 2; Length 648
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL. BX294136; CAD72348.1; -
Complete Protocone; Hypothetical protein.
SEQUENCE 648 AA; 73073 MW; SEBTAILAR4501263 CRC64;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
DNA-directed RNA polymerase subunit L (EC 2.7.7.6).
Mame-rpol, OrderedLocusNames=MK0058;
Methanopyrus kandleri.
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                                                                                          STRAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=1027-647; Bubbde=11930014; DOI=10.1073/pnas.032671499;
Slearev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Koozyavkin S.A.; Wolf Y.I., Stetter K.O., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
Proc. Natl. Acd. Sci. U.S.A. 99:4644-4649(2002).
-- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                            (KNA)(N).
SIMILARITY: Belongs to the archaebacteria RPOL / eukaryotic RPB11/
RPC19 RNA polymerase subunit family.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyrus.
Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                        substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00261; -; 1.
InterPro; IPR009025; RNAP_RBP11-like.
InterPro; IPR008193; RNAP_Rpb11_L.
Pfam; PF01193; RNA_PO1_L; JND; FALSE_NEG.
PROSITE; PS01154; RNA_POL_L, JND; FALSE_NEG.
Complete proteome; DNA-directed RNA polymerase; Transcription;
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Matches 10, Conservative
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SEQUENCE 1
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Search completed: November 10, 2004, 12:27:12 Job time: 24.8827 secs

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Sequence 4166, Ap
Sequence 27, Appli
Sequence 10, Appli
Sequence 7, Appli
Sequence 26, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
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Sequence 6023, Ap
Sequence 6, Appli
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Sequence 50573, A
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(GGDZ 6/ptodata1/liaa/5A_COMB.pep:*
/GGDZ 6/ptodata1/liaa/5B_COMB.pep:*
/GGDZ 6/ptodata1/liaa/6A_COMB.pep:*
/GGDZ 6/ptodata1/liaa/6B_COMB.pep:*
/GGDZ 6/ptodata1/liaa/6B_COMB.pep:*
/GGDZ 6/ptodata1/liaa/BCTUS_COMB.pep:*
/GGDZ 6/ptodata1/liaa/backflles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-583-110-4166
US-08-221-364A-8
US-08-221-364A-8
US-09-233-98-10
US-09-538-092-7
US-09-511-164-40
US-09-51-1064-40
US-09-270-76-35356
US-09-270-76-35356
US-09-270-76-35356
US-09-270-76-35356
US-09-270-76-35356
US-09-270-76-35356
US-09-270-76-35356
US-09-22-617A-2
US-08-222-617A-2
US-08-223-617A-2
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1 TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
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-09-489-039A-11817
T-US96-11445-8
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US-09-252-991A-27758
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
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Sequence 7838, Ap	Sequence 2, Appli	Sequence 36, Appl	Sequence 18997, A	Sequence 4, Appli		Sequence 42243, A		Sequence 4086, Ap	8, A	ς,	Sequence 8, Appli	ດັ	ď	۳ ش	455	22263	Sequence 183, App
US-09-328-352-7838	US-08-591-079-2	US-08-637-670-36	US-09-248-796A-18997	US-08-551-459-4	US-09-248-796A-22798	US-09-270-767-42243	US-09-270-767-57522	US-09-107-532A-4086	US-08-762-106-8	US-08-745-404-2	US-09-320-774-8	US-08-762-106-9	US-09-320-774-9	US-08-745-404-3	US-09-543-681A-4556	US-09-252-991A-22263	US-08-755-587-183
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26.4	26.4	26.4	26.4	26.4	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1
47	47	47	47	47	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5
28	50	30	31	32	33	34	35	36	37	38	რ	40	41	42	43	44	4 5

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Sequence 4, Application US/09110517A
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Sequence 10. 6248520
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Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 32; Conservative 0; Mismatches 0; Indels
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CRGANISM: Homo sapiens
US-09-110-517-4
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697 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 728

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Fri Nov 12 14:54:52 2004

ö Gaps . 0 Sequence 8, Application US/08271364A
Patent No. 5756334
GENERAL INFORMATION:
APPLICANT: PERLEX, FRANCINE B.
APPLICANT: SOUTHWORTH, MAURICE W.
TITLE OF INVENTION: RECOMBIRANT THEROWSTABLE DNA POLYMERASE
TITLE OF INVENTION: FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW BRIGLAND BIOLABS, INC. DB 4; Length 88; 5; Indels WEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
ODFRAHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/21,364A
FILING DATE: US/08/21,364A
FILING APPLICATION DATA:
APPLICATION DATA: US/08/340
FILING APPLICATION DATA:
APPLICATION DATE: 18-DEC-1991
FILING APPLICATION DATA:
APPLICATION DATE: US/086,340
FILING DATE: 17-AFR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-AFR-1990
PRIOR APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-AFR-1990
PRIOR APPLICATION NUMBER: US 07/513,994
FILING DATE: 36-AFR-1990
PRIOR APPLICATION NUMBER: US 07/513,994 Query Match
29.8%; Score 53; DB 4
Best Local Similarity 45.0%; Pred. No. 2.4;
Matches 9; Conservative 6; Mismatches REFERENCE/DOCKET NUMBER: NE TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 927-5054 TELEFAX: (508) 927-1705 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: unknown , MOLECULE TYPE: protein US-08-271-364A-8 ZIP: 01915 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (unknown amino acid STRANDEDNESS: RESULT 3 US-08-271-364A-8 d

942 YSNLIP-----KEILRDVFGKEFQK 961

'n Length 1022; PATENT NO. 2834285

GENERAL INFORMATION:
APPLICANT: Comb, Donald G.
APPLICANT: Comb, Donald G.
APPLICANT: Comb, Donald G.
APPLICANT: Maliam E.
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
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ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
ADPLICATION NUMBER: US/08/22,715B
FILING DATE: 04-APR-1994 Indels DB 2; 4; Mismatches Score 51.5; Pred. No. 66 NAME: Williams, Gregory D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-054C3FC2
TELECOMMULCATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705 CLASSIPLECATION: 535
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,238
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
ATTORNEY/AGEN INFORMATION: Sequence 27, Application US/08222715B Patent No. 5834285 Query Match
Best Local Similarity 44.0%;
Matches 11; Conservative 1022 amino acids ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-222-715B-27 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1022 amino aci TYPE: amino acid STRANDEDNESS: un RESULT 4 US-08-222-715B-27

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Gaps

RESULT 5 US-09-233-989-10

Gaps

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Score 51.5; DB 1; Length 1022; Pred. No. 66; 4; Mismatches 5; Indels 5;

Query Match
Best Local Similarity 44.0%;
Matches 11; Conservative

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RESULT 8
US-09-640-419C-20
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                                                                  APPLICANT: Chen, Hong
APPLICANT: Mayer, Joanne
APPLICANT: Mayer, Joanne
TITLE OF INVENTION: Method of Detecting Risk of Type II Diabetes Based on
TITLE OF INVENTION: Mutations Found in Carboxypeptidase E
FILE REFERENCE: 5800-14 038800/174130
CURRENT APPLICATION UNMER: US/09/233,989
CURRENT PILING DATE: 1999-10-19
EARLIER APPLICATION NUMBER: 60/105,102
SAPLIER PILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
ILENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09538092
| Sequence 7, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Giot, Loid
| APPLICANT: Mansfield, Traci A. |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: 15966-542 |
| CURRENT FILING DATE: 10900-03-29 |
| PRIOR FILING DATE: 1999-04-01 |
| PRIOR FILING DATE: 2000-02-01 |
| NUMBER OF SEQ ID NOS: 1387 |
| SOFTWARE: CuraPatSeqFormatter Version 0.9 |
| SEQ ID NO 7 |
| LENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.7%; Score 51; DB 3; Length 641; Best Local Similarity 38.7%; Pred. No. 46; Matches 12; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature; LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number YAR003W US-09-538-092-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: carboxypeptidase homolog -- CPZ
US-09-233-989-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 YWRLLPPGIHIVIAQAPGYAKVIKKVIIPAR 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSR 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 467, Application US/09711164
Patent No. 6589738
APPLICANT: Forsyth, R. Allyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces cerevisiae
Sequence 10, Application US/09233989
Patent No. 6248527
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%;
Matches 9; Conservative
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US-09-711-164-467
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APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETC
FILE REPERENCE: ELITRA.008A.
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR RILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 467
LENGTH: 1377
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Patent No. 6630615

GENERAL INFORMATION:

APPLICANT: Bidney, Dennis L

APPLICANT: Lu, Guinua

APPLICANT: Lu, Guinua

APPLICANT: Lu, Guinua

APPLICANT: Lu, Guinua

APPLICANT: Lu, Guinua

TILE REFERENCE: 35718/199009 (5718-92)

CURRENT APPLICATION NUMBER: US/09/640,419C

CURRENT APPLICATION NUMBER: 60/149,656

FRIOR PELING DATE: 1999-08-18

FRIOR PELING DATE: 1099-08-18

FRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 20

LENGTH: 595
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HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATE:
PLING DATE: 03-31-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
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;Patent No. 5223423
PAPLICANT: FRANCHINI, GENOVEFFA;WONG-STAAL, FLOSSIE;
;GALLO, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.1%; Score 50; DB 4;
Best Local Similarity 42.3%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.8%; Score 49.5; Best Local Similarity 52.2%; Pred. No. 65 Matches 12; Conservative 3; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261 PKSPAQQQADDNAAKALTKWWNDTAS 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PKRPIKEVLTDIFAKVLEKGWVDSRS 33
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Escherichia coli
US-09-711-164-467
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RESULT 13
US-09-328-352-6023
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 6609
LENGTH: 155
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM:
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US-09-270-767-50573
Sequence 50573, Application US/09270767
Sequence 50573, Application US/09270767
Sequence 50573
Sequence 50573
Sequence 50573
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION Nucleic acids and proteins of Drosophila melanogaster;
CURRENT PELICALION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NOS: 62573
LENGTH: 145
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       Length 3077;
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                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
Score 49.5; DB 6;
Pred. No. 4.5e+02;
1; Mismatches 3;
                                                                                                                                                                                                                 1585 YWNLTP------EKGWLSSYS 1599
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                                                                                                                                               33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; FORMATION: Xaa means any amino acid
VS-09-270-767-35356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB
Pred. No. 16;
5; Mismatches
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                                                                                                                                               2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS
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; Sequence 6609, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
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       27.8%;
34.4%;
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27.5%;
Best Local Similarity 45.5%;
Matches 10; Conservative 5
Query Match
Best Local Similarity 34.4*
Matches 11; Conservative
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Patent No. 566293, Application US/09328352

Sequence 6023, Application US/09328352

Patent No. 566294

Patent No. 566294

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6023
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BYTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 031796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT PILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR PILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTHWARE: PATENTING DATE: 1937-08-15 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: veenstra, Annemarie E.
APPLICANT: Matchi, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Van Liempt, Hans
APPLICANT: Van Liempt, Henk
APPLICANT: Wontenegro, Eduado P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Authbiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 4;
Pred. No. 18;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | || : :|| :|||
PYEPIIDKAMEIFEHCMEQGWV 310
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US-08-222-617A-6
Sequence 6, Application US/08222617A
Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PKRPIKEVLTDIFAKVLEKGWV
                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Enterococcus faecalis
US-09-134-000C-6609
                                                                                                                                                                                                                                                                                                                                                                                                                                   27.5%;
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Best Local Similarity 40.9%
Matches 9; Conservative
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Matches 9; Conservative
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LOCATION: 1..3666
OTHER INFORMATION: /label= region
OTHER INFORMATION: /note= "Region of ACV Synthetase; aa 62-3727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 10, 2004, 12:32:29 Job time: 10.8287 secs
            US/08/222,617A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
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APPLICALL.
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,1
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
**FNGTH: 3666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: Protein
LOCATION: 1..3666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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APPLICANT: Wartin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Gruno D.
APPLICANT: Barredo, Jose L.
APPLICANT: Barredo, Jose L.
APPLICANT: Van Liempt, Henk
APPLICANT: Van Liempt, Henk
APPLICANT: Van Liempt, Henk
APPLICANT: Wontenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Domain II
/note= "Domain II of ACV Synthetase from
Penicillium chrysogenum; aa 1397-2154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 27.5%; Score 49; DB 2; Length 758; Best Local Similarity 40.9%; Pred. No. 1.18+02; Matches 9; Conservative 8; Mismatches 5; Indels
                                                                                                                                             ZLI: buouc

COMPUTER: ELDEPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC.Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUBER: US/08/22,617A

FILING DATE: 04-APR.1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 97,157

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENGTH: 758 anino acids

TYPE: anino acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSER: _McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Penicillium chrysogenum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 DVVPPRSEIERSLCDIWAELLE 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NLLPPKRPIKEVLTDIFAKVLE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain
LOCATION: 1..758
GOTHER INFORMATION:
COTHER INFORMATION:
GOTHER INFORMATION:
COTHER INFOR
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                Chicago
Illinois
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US-08-222-617A-12
                                                                                       COUNTRY:
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Gaps

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RESULT 2
US-10-435-696-40
Sequence 40, Application US/10435696
Publication No. US20040018525A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Appl
Sequence 64, Appl
Sequence 112003,
Sequence 112000,
Sequence 271602,
Sequence 271602,
Sequence 14954, A
Sequence 162349,
Sequence 267928,
Sequence 267928,
Sequence 267928,
Sequence 267928,
                                                                                                            November 10, 2004, 15:53:52; Search time 31.8287 Seconds (without alignments) 366.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. (cgn2_6)ptodata/1/pubpaa/US07 PUBCOMB.ppp:*
2. (cgn2_6)ptodata/1/pubpaa/US07 PUBCOMB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US07 NEW PUB.ppp:*
4. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
5. (cgn2_6)ptodata/1/pubpaa/US07 NEW PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US07 NEW PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US07 NEW PUB.ppp:*
7. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
9. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
11. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
12. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
12. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
12. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
13. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
14. (cgn2_6)ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
15. (cgn2_6)ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
16. (cgn2_6)ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
17. (cgn2_6)ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
18. (cgn2_6)ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
19. (cgn2_6)ptodata/1/pubpaa/US106_NEW_PUB.ppp:*
19. (cgn2_6)ptodata/1/pubpaa/US106_NEW_PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-435-696-40
US-10-437-963-1123003
US-10-437-963-1123003
US-10-437-993-171900
US-10-437-993-171900
US-10-369-493-14462
US-10-369-493-14462
US-10-369-493-14662
US-10-437-963-162349
US-10-437-963-162349
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US-10-437-963-162349
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US-10-437-963-162349
US-10-437-963-162349
US-10-437-963-121335
                                                                                                                                                                                         US-10-092-750-16
178
1 TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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    protein search,

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Match
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Perfect score:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                             OM protein
                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                  Run on:
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quence 13194	equence 737	equence 1733]	205,	equence 285,	equence 1211	24648	equence 67796	14654	equence 14808	25743	equence 1	equence 10324	Seguence 77684	0, App	104,	Sequence 43276, A	45466	1945	Sequence 52042, A	e 58607	31682	25216	190	equence 838,	15420	ednence	121	equence 4823	298,	a)	Sequence 10384, A
115-242	282-122A-73	437-963-17331	032-214-20	032-214-285	437-963-12113	424-599-24	.282-122A-6779	437-963-14654	437-963-14808	425-115-25743	437-963-16307	437-963-103	2-122A-7768	327-040-1	757-262-	425-114-432	425-114-45466	-425-115-194	425-1	425-114-58607	425-115-31682	424-599-2521	437-963-19021	389-566-838	.437-963-	-389-566-	437-96	-767-701-4823	-686-947-	-437-963-	US-09-815-242-10384
σ	15	16	14	14	16	12	15	16	16	17	16	16	15	σ	17	15	15	17	15	15	17	15	76	15	16	15	16	16	16	16	σ
88	88	95	303	303	1199	217	722	73	856	85	86	88	155	641	641	662	888	967	970	970	1472	145	429	537	598	614	1286	61	518	972	1377
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14	15	16	17	18	19,	20	21	22	23	24	25	26	. 27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	4.5

ALIGNMENTS

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Gaps
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US-10-092-750-16

Sequence 16, Application US/10092750
Publication No. US2003003157A1
Publication No. US2003003157A1

APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia

TILB OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REPERENCE: 50036/050002,
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT PILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/07/050
NUMBER OF SEQ ID NOS: 253

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PELSER OF Windows Version 4.0

LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 178; DB 14; 1 Similarity 100.0%; Pred. No. 3.4e-17; 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 33; Conserv
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-2153221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WS-10-424-599-171900

WITHE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: WIMPER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53233)8
CURRENT APPLICATION NUMBER: US/10/424,599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.8%; Score 62; DB 16; Length 102; Best Local Similarity 40.0%; Pred. No. 1.2; Matches 10; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12623C.1.pep
US-10-424-599-171900
                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT4530_1592C.1.pep US-10-437-963-112003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.0%; Score 57; DB 15; Best Local Similarity 45.5%; Pred. No. 10; Matches 15; Conservative 5; Mismatches 9
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LOCATION: (1)..(102)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TYWNLL---PPKRPIKEVLTDIFAKVLEKGWVD 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YWNLLPPKRPIKEVLTDIFAKVLEK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 YWRLPPPRRLVEELPGDLSEKIVEE 51
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
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US-10-424-599-271602
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                                                                                               DIAGNOSIS, PROGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 54304, Application US/10767701
Publication No. US20040172684A1
Publication No. US20040172684A1
Publication No. US20040172684A1
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Shouleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Number: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NOS: 63128
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        ## APPLICANT: Wirtz, Ralph
## APPLICANT: Winte, Marc
## APPLICANT: Wintes, Marc
## APPLICANT: Wintes, Marc
## APPLICANT: Wallabis, Harald
## TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSI
## TITLE OF INVENTION: PREVENTION PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
## TITLE OF INVENTION: PREVENTION NUMBER: US/10/435,696
## CURRENT APPLICATION NUMBER: US/10/435,696
## PRIOR PILING DATE: 2003-05-03
## PRIOR PILING DATE: 2003-02-13
## PRIOR PILING DATE: 2003-05-13
## PRIOR PILING DATE: 2003-05-21
## NUMBER OF SEQ ID NOS: 314
## SOFTWARE: Patentin version 3.1
## SEQ ID NO 40
## LENGTH: 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.2%; Score 173; DB 15; Length 989; 100.0%; Pred. No. 7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: 14513462.pep
US-10-767-701-54304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112003, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Boukharov, Andrey A.
Barbazuk, Brad
Li, Ping
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckarov, Andrey A
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
// ORGANISM: Homo sapiens
US-10-435-696-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-10-369-493-14462

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Sequence 11629, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.2%;
37.1%;
                                                     Query Match
Best Local Similarity 42.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Sequence 14462, Application US/10369493

Sequence 14462, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Goo, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goodman, Barry S.
APPLICANT: Goodman, Barry S.
APPLICANT: Goodman, Barry S.
APPLICANT: Goodman, Barry S.
APPLICANT: Goodman, EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14462

LENGTH: 282

TENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7

US-10-369-493-14954

US-10-369-493-14954

Sequence 14954, Application US/10369493

Publication No. US2030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-21

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 277
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                  ; FEATURE:

1 OTHER INFORMATION: Clone ID: PAT_MRT3847_87276C.1.pep

US-10-424-599-271602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LLPPKR-----PIKEVLTDIFAKVLE--KGWVD 30
                                                                                                                                                                                                                                                                                                                                                                   28 YWKSVLPTTPMPKAITDI----LYSDWVEEKS 55
                                                                                                                                                                                                                                                                                                                                     2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
31.2%; Score 55.5; Di
Best Local Similarity 42.9%; Pred. No. 28;
Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                Query Match 31.5%; Score 56; DB Best Local Similarity 34.4%; Pred. No. 30; Matches 11; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14954
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 271602
LENGTH: 341
                                                                                  TYPE: PRT ORGANISM: Glycine max
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Sequence 162348, Application US/10437963
; Sequence 162348, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brazaruk, Brad
; APPLICANT: Brazaruk, Brad
; APPLICANT: Ding US Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162348
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Barry S.
APPLICANT: Gregory J.
APPLICANT: Gregory J.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING NATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11629
LENGTH: 495
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31.2%; Score 55.5; DB 14; Length 282; 42.9%; Pred. No. 28;
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Pred. No. 1.1e+02;
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US-10-437-963-162348
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                                                                                                                                                                                                    118 LIPPTRILDLRKDPAGKPLKPVFAKAFEYSDGWVD 152
                                                                                                                                  5 LLPPKR-----PIKEVLTDIPAKVLE--KGWVD 30
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31.2%; Score 55.5; D
Best Local Similarity 42.9%; Pred. No. 53;
Matches 15; Conservative 2; Mismatches
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Scoulic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Yamanoco, Robert T.
APPLICANT: Yamanoco, Robert T.
APPLICANT: Yamanoco, Robert T.
APPLICANT: Yamanoco, Robert T.
APPLICANT: Xu, H. Howar, Brokaryotes
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-11.4
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-01-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-26
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
NUMBER: PSEQ ID NOS: 14110
SSEQ ID NO 13194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 YWNLLPPKRPIKEVLTDIFA----KVLEKG------WVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: PAT_MRT4530_24190C.1.pep
US-10-437-963-121135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.5; 1
Pred. No. 27;
                                                                                                                   Sequence 121135, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13194, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-815-242-13194
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT FILING DATE: 2003-05-14*
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 202829
TYPE: LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBERS. 38-21(33.22)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 26'928
LENGTH: 109
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llarity 37.5%; Pred No. 39; 7; Indels
Conservative 8; Mismatches 7; Indels
Indels
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US-10-437-963-202829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Clone ID: MRT4577_175952C.1.pep
US-10-425-115-267928
                                                                                                           2 YWNLLPPKRPIKEVLTDIF----AKVLEKGWVDS 31
6; Mismatches
                                                                                                                                                                                                                                                                                               Sequence 267928, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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52 VPPKRPVPIALFNSWASLLERG 73
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Conservative
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ORGANISM: Oryza sativa
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JS-10-425-115-267928
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29.8%; Score 53; DB 15; Length 88;
Best Local Similarity 45.0%; Pred. No. 17;
Matches 9; Conservative 6; Mismatches 5; Indels
                                            Query Match

29.8%; Score 53; DB 9; Length 88;
Best Local Similarity 45.0%; Pred. No. 17;
Matches 9; Conservative 6; Mismatches 5; Indels
                                                                                                                                            ; Sequence 73718, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT;
CRGANISM: Streptococcus pneumoniae
US-10-282-1228-73718
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13194
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17 KKEISETLTDVYASLNDKGY 36
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9 KRPIKEVLTDIFAKVLEKGW 28 | . . | | | | | | | : : | | : | | : | | 17 KKEISETLTDVYASLNDKGY 36

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Search completed: November 10, 2004, 16:36:00 Job time: 32.8287 secs

Oden Mole ecolemia

us-10-092-750-16.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51 Run on:

; Search time 6.6713 Seconds (without alignments) 475.942 Million cell updates/sec

US-10-092-750-16 Title: Perfect score:

178 1 TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	:	hypothetical prote	hypothetical prote	glycerol-3-phospha	folowou.eues pals	RNA binding protei	conserved hypothet	hypothetical prote	_	_	platelet-derived g	probable polyketid	vif protein - huma	protein -	DNA-directed DNA p	conserved hypother	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	enterobactin synth	cdtC protein - Esc	ц	signal-transducing	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	phosphoenolpyruvat	rhsA protein in rh	rhsA protein precu
SUMMARIES	ID	538165	D69438	AH2996	A98287	S58155	D95022	G97893	B37842	AF1987	S44269	B70588	ASLJGG	S12154	S42459	A82390	S18240	QYNT	528614	JH0667	E69615	169096	840901	H69305	4	-	7	N	E86034	6515
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RESULT 2
D69438
hypothetical protein AF1509 - Archaeoglobus fulgidus
CiSpecies: Archaeoglobus filgidus
CiSpecies: Archaeoglobus filgidus
CiSpecies: Archaeoglobus filgidus
CiSpecies: Archaeoglobus filgidus
CiSpecies: D6-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
CiAccession: D69438
CiStron E09438
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CDA peptide synthe	pristinamycin I sy	vif protein - huma	vif protein - huma	hypothetical prote	transcription fact	hypothetical prote	hypothetical prote	phosphoenolpyruvat	hypothetical prote	phosphoenolpyruvat	hypothetical prote	phosphoenolpyruvat	phosphoenolpyruvat	microcystin synthe	alpha-aminoadipyl-
T36180	T30289	ASLJS2	ASLJSW	T04438	T46894	E90189	843354	PC2168	T31587	PC2169	T01527	840304	T52186	AH2136	YGPLV3
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30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

× , , ,	RESULT 1 \$38165 hypothetical protein YKR087c - yeast (Saccharomyces cerevisiae) NAlternate names: hypothetical protein YKR407 C;Species: Saccharomyces cerevisiae C;Date: 03-May-1994 #sequence revisiae C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: \$38165; \$42016; \$39128 R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo, submitted to the Protein Sequence Database, March 1994 A;Reference number: \$38158 A;Accession: \$38165 A;Accession: \$38165 A;Accession: \$38165 A;Residues: 1-314 <abal> A;Residues: 1-314 <abal> A;Cross-references: UNIPROT:P36163; EMBL:Z28312; NID:g486604; PIDN:CAA82166.1; PID:g48660</abal></abal>
	Ajaxperimental Bource: Bergain 5200C Vacarcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha, M.A. Yeast 10, 231-245, 1994 A;Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromo A;Reference number: S42009; MUID:94262327; PMID:8203164 A;Molecile type: DNA
	A; Residues: 1.7Fu - CAR> A; Residues: 1.7Fu - CAR> A; Cross-references: EMBL: Z27116; NID: g415899; PIDN: CAA81638.1; PID: g415907 A; Experimental source: strain S288C C; Genetics: C; Genetics: SGD: S0001795 A; Map position: 11R
	ransmembrane protein ain: transmembrane #s
	Query Match 32.0%; Score 57; DB 2; Length 314; Best Local Similarity 33.3%; Pred. No. 4.8; Matches 10; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
	Oy 1 TYWNLLPPKRPIKEVLJDIFAKVLEKGWVD 30 : : :: : : B6 TQQEILPPQHPLSIKIENIFWKIVEAAYKD 115

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A,Accession: T38559
A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Molecule type: DNA
A,Roelduse: 1-529 cGE2>
A,Cross-references: UNIPROT:009702; EWBL:ZS0142; NID:g1052783; PIDN:CAA90498.1; PID:g1055
A,Experimental source: strain 972h(-); cosmid c2P7
R,Eukshara, K.; Yanamoto, H.; Okayam, H.
Mol. Cell. Biol. 18, 4488-4498, 1998
Mol. Cell. Biol. 18, 4488-4498, 1998
A,Atitle: An RNA binding protein negatively controlling differentiation in fission yeast.
A,Reference number: Z25070; MUID:98136254; PMID:9671488
A,Accession: T50458
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A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Description: functions as negative regulator of differentiation, blocks the onset of ch a critical level of starvation [validated, WUID:98336254]
A,Note: preferentially binds poly(U)
F;207-265/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                                                                                                                                                                 SSBISS
RNA binding protein Nrdl [validated] - fission yeast (Schizosaccharomyces pombe)
RNA binding protein Nrdl [validated] - fission yeast (Schizosaccharomyces pombe
C;Species: 13-Jan-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: T38559; T50458; SSB155
C;Accession: T38559; T50458; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
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                                                                                                    137 LLPPTRTLDLRKDPAGKPLKPVPAKAFEYSDGWVD 171
                                                      S LLPPKR-----PIKEVLTDIFAKVLE--KGWVD 30
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ilarity 35.7%; Pred. No. 16;
Conservative 5; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA; Residues: 1-529 <TSU>
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5
        Conservative
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A;Molecule type: DNA
A;Residues: 1-88 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-515 «KUR»
/cross-references: UNIPROT: Q8U9Z7; GB:AE008689; PIDN:AAL44390.1; PID:g17741987; GSPDB:G
/Bxperimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gispecies: Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul=2004
C;Accession: Age287
B;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Ritle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MulD:21608551; PMID:11743194
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A;Molecule type: DNA
A;Residues: 1-531 «KUUR»
A;Cross-references: UNIPROT:Q8U927; GB:AE007870; PIDN:AAK89819.1; PID:g15159751; GSPDB:G
                                                                                                                A;Residues: 1-262 <KLE>
A;Cross-references: UNIPROT:028763; GB:AE000998; GB:AE000782; NID:g2689321; PIDN:AAB8974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycerol-3-phosphate dehydrogenase glpD [imported] - Agrobacterium tumefaciens (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eer, B.W.
Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
Reference number: AB2577; MUID:21608550; PMID:11743193
Accession: AH2996
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                    A;Accession: D69438
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-262 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                          / Match 31.5%; Score 56; DB 2; Length 262; Local Similarity 44.0%; Pred. No. 5.4; Onservative 5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
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A;Map position: linear chromosome
C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map podition: linear chromosome C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)
              A; Reference number: A69250; MUID: 98049343; PMID: 9389475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 31.2%; Score 55.5; Di 1 Similarity 42.9%; Pred. No. 13; 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.2%; Score 55.5; I 42.9%; Pred. No. 14;
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TYFNFFPPKQPIQ--MTDTAGNTVE 212
                                                                                                                                                                                                                                                                                                             1 TYWNLLPPKRPIKEVLTDIFAKVLE 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: AH2996
                                                                                                                                                                                                      Query Match
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Best Local
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Matches
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Diatelet-derived growth factor receptor alpha - zebra fish (fragment)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S44269
R;Yu, W.; Richardson, W.D.
Submitted to the EMBL Data Library, April 1994
Submitted to the EMBL Data Library, April 1994
A;Peccession: S44269
A;Accession: S44269
A;Reference number: S44269
A;Reference number: S44269
A;Rocession: S44269
A;Rocession: 4457 <VUW>
A;Reference under: S44269
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology; C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology; C;Superfamily: macrophage colony-stimulating factor 1 receptor; phospip. F;1-327/Domain: protein kinase homology (fragment) <KIN>
DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Rocession: AF1987
A,Status: preliminary
A,Molecule type: DNA
A,Residus: 1-192 <KUR>
A,Residus: 1-192 <KUR>
A,Cross-references: UNIPROT:P29979; GB:BA000019; PIDN:BAB73406.1; PID:g17130796; GSPDB:GPA; Cross-references: Strain PCC 7120
G,Genetics:
A,Genetics:
A,Gen
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A;Cross-references: UNIPROT:005819; GB:Z95208; GB:AL123456; NID:g3261747; PIDN:CAB08474.1
A;Experimental source: strain H37Rv
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C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable polyketide synthetase mbtF [similarity] - Mycobacterium tuberculosis (strain H37 C,Species: Mycobacterium tuberculosis
C,Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyaccesion: B70588
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
Ayauthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: B70588
A; Status: preliminary: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 2; Length 192;
Pred. No. 13;
6; Mismatches 12; Indels
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WNLLPPKRPIKEVLTDIFAKVLEKGW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%;
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1 Similarity 37.9%;
11; Conservative
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Best Local Similarity
Matches 11; Conserva
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C;Superfamily
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AP1987

AP1987

Apportetical protein alr1449 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AF1987

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8C289; GB:AE007317; PIDN:AAK98979.1; PID:g15457718; GSPDB:G
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-164 <LAM>
A;Cross-references: UNIPROT:P29979; GB:U38537; GB:M38044; NID:g1053082; PIDN:AAC82966.1;
C;Superfamily: Anabaena hypothetical protein 2 (xisA 3' region)
                                                                                                                                                                                                                                                                                             RESULT 7
(97893
hypothetical protein spr0175 [imported] - Streptococcus pneumoniae (strain R6)
c;Species: Streptococcus pneumoniae
c;Date: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004
C;Accession: G97893
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
P. R; LeBlanc, D.J.; Lee, L.W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Atthors: Vang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97893
A;Accession: G97893
A;Accession: G97893
A;Ascelus: preliminary
A;Molecule type: DNA
A;Residues: 1-88 KURA
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B37842.

hypothetical protein 2 (xisA 3' region) - Anabaena sp. (strain PCC 7120)
c;Species: Anabaena sp.
c;Species: Anabaena sp.
c;Date: 21-Jun-1991 #sequence_revision 21-Jun-1991 #text_change 09-Jul-2004
c;Accession: B37842
F;Lammers, P.J.; McLaughlin, S.; Papin, S.; Trujillo-Provencio, C.; Ryncarz II, A.J.
J. Bacteriol. 172, 6981-6990, 1990
A;Title: Developmental rearrangement of cyanobacterial nif genes: nucleotide sequence, A;Reference number: A37842; MUID:91072249; PMID:2123860
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Pred. No. 11;
6; Mismatches 12; Indels
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                                                  Indels
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Pred. No. 4.1;
           Pred. No. 4.1;
6; Mismatches
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                                                                                                                                                                17 KKEISETLTDVYASLNDKGY 36
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                                                                                                                     KRPIKEVLTDIFAKVLEKGW 28
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Local Similarity 37.9%;
hes 11; Conservative
       Similarity 45.0%;
9; Conservative
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Best Local Similarity 45...
Best Jocal 9; Conservative
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A; Residues: 1-1702 <PERI>
A; Residues: 1-1702 <PERI>
A; Cross-references: UNIPROT: B30317; EMBL:M74198; NID: g154685; PIDN: AAA72100.1; PID: g15468
B; Perier: R.B.; Comb. D.G.; Jack, W.E.; W.E.; W.E.; Qiang, B.; Kucera, R.B.; Benner, J.; Proc. Natl. Rcad. Sci. U.S.A. 89, 5577-5581, 1992
A; Title: Intervening sequences in an Archaea DNA polymerase gene.
A; Reference number: $42450; MUID: 92302285; PMID: 1608969
A; Residues: 181-222; 387-425; 452-476; 483-524; 1021-1062; 1076-1099; 1466-1489; 1533-1547 <PER; A; Residues: 181-222; 387-425; 452-476; 483-524; 1021-1062; 1076-1099; 1466-1489; 1533-1547 <PER; A; Residues: EmBL:M74198
B; Hodges, R.A.; Perler, F.B.; Noren, C.J.; Jack, W.E.
Nucleic Acids Res. 20, 6153-6157, 1992
A; Reference number: Splicing removes intervening sequences in an archaea DNA polymerase.
A; Reference number: squ'988; MUID: 93117083; PMID: 4475179
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Description: endonuclease, hydrolase
A; Note: DNA endonuclease PI-T111
A; Note: DNA endonuclease PI-T111
C; Superimanly: Thermococcus literalis DNA-directed DNA polymerase Vent
C; Superimanly: Thermococcus literalis DNA-directed DNA polymerase Vent #status predicted
C; Superimanly: DNA-binding; endonuclease; hydrolase; nucleotidyltransferase; protein splicir
F; 1-494, 1033-1081, 1472-1702/Product: DNA-directed DNA polymerase Vent extein 1 #status predicted <NT1>F; 1494-1033/Product: DNA-directed DNA polymerase Vent extein 2 #status predicted <NT2>F; 1033-1081/Domain: DNA-directed DNA polymerase Vent extein 2 #status predicted <NT2>F; 1032-1471/Product: DNA endonuclease PI-II (pol Vent intein 2) #status predicted <NT2>F; 1472-1702/Domain: DNA-directed DNA polymerase Vent extein 3 #status predicted <NT3>F; 494-1033/Cross-link: peptide (Asp-Ehr) #status predicted
F; 1081-1472/Cross-link: peptide (Asp-Thr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-155 <HEI>
A,Cross-references: UNIPROT:09KKTB; GB:AE004427; GB:AE003853; NID:99658442; PIDN:AAF96906
A,Experimental source: serogroup O1; strain N16961; blotype El Tor
C,Genetics:
DNA-directed DNA polymerase (EC 2.7.7.7) Vent, intein containing precursor - Thermococcus N. Contains DNA endomuclease (EC 3.1.-..) PI-I; DNA endomuclease (EC 3.1.-..) PI-II; DNA-C;Species: Thermococcus litoralis
C;Date: 31-Dec-1993 #sequence revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: 48459; 84451; 842451; 842450; 843488
R;Perler, F.B.; Comb. D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Benner, J.S. submitted to the EMBL Data Library, September 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein VCA1012 [imported] - Vibrio cholerae (strain N16961 serog1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82390
C;Accession: A82390
R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD: 20406833; PMID: 10952301
A;Accession: A82390
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.9%; Score 51.5; DB 2; Length 1702; 44.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              942 YSNLIP----KEILRDVFGKEFQK 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YWNLLPPKRPIKEVLTDIFAKVLEK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: nucleotidyltransferase A; Note: DNA-directed DNA polymerase Vent C; Function: <END1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Description: endonuclease, hydrolase A,Note: DNA endonuclease PI-Tli1 C; Function: <END2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                      A, Reference number: S42458
A, Accession: S42459
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function: <VENT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 18-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 512154
R;Kuehnel, H.; Kreutz, R.; Ruebsamen-Waigmann, H.
Nucleic Acids Res. 18, 6142, 1990
A;Title: Nuclectide sequence of HIV-2(D194), an isolate from a Gambian case of 'Neuro-Al A;Reference number: 512152; MUID:91045094; PMID:2235509
A;Accession: 512154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; nucleic acid sequence not shown, translation not shown A,Status: preliminary; nucleic acid sequence not shown, translation not shown A,Molecule type: DNA A,Residues: 1-212 «KUDA A,Residues: 1-212 «KUDA A,Cross-references: UNIPROT:P17758; EMBL:X52223; NID:g60155; FIDN:CAA36466.1; PID:g60158 A,Notes: the nucleotide sequence was submitted to the EMBL Data Library, June 1990 C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "If protein - human immunodeficiency virus type 2 (isolate GH-1)

NyAlternate names: orf-Q protein; sor protein

C;Species: human immunodeficiency virus type 2, HIV-2

A;Note: host Homo sapiens (man)

C;Accession: JS0329

G;Accession: JS0329

A;Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence

A;Reference number: JS0327; MJD: 90122350; PMID: 2611042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:P18043; GB:M30895; GB:D00477; NID:g325709; PIDN:AAA43934.1; A;Note: this sequence was submitted to JIPID, October 1989 C;Genetics: Afgene: vif A,Gene: vif C;Superfamily: AIDS vif protein C;Keywords: AIDS; immunodeficiency
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        F;517-949/Domain: acetate-CoA ligase homology <ACL>
F;964-1031/Domain: acyl carrier protein homology <ACP>
F;996/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 215;
                                                                                                                                                             Length 1461,
                                                                                                                                                         Score 52; DB 2; Length 146
Pred. No. 1.3e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EKGWLSSHS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51.5; DB
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.9%; Score 51.5; D
34.4%; Pred. No. 18;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          961 PPQTPTELVLAEAFADVMETSNVD 984
                                                                                                                                                                                                                                                                                                                  7 PPKRPIKEVLTDIFAKVLEKGWVD 30
                                                                                                                                                                 29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.9%;
ilarity 34.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 34.4%;
nes 11; Conservative
                                                                                                                                                                                                     Best Local Similarity 45.8 Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-215 < HAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: JS0329
                                                                                                                                                                     Query Match
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S42459
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A,Gene: VCA1012
A,Map position: 2
C,Superfamily: spore maturation protein, SpmB type
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0; Gaps Query Match
28.7%; Score 51; DB 2; Length 155;
Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 4; Indels

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13 KEVLTDIFAKVLEKGWV 29 | ::|||| : :|||| 8 KPMVTDIFVEGAKKGWV 24

ð g Search completed: November 10, 2004, 12:29:20 Job time : 7.6713 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:27:01; Search time 36.1065 Seconds (without alignments) 525.871 Million cell updates/sec Run on:

US-10-092-750-16 178 1 TYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:** Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O8r004 mus musculu	mus	3 h th	1 mu	Q6pi53 xenopus lae	Aah43802 xenopus 1	Q6nuw0 brachydanio	Aah68408 brachydan	O9n4t2 caenorhabdi				Q6m0e9 methanococc	7	Q8mmb8 drosophila		Q6xa09 alternaria	Aap78735 alternari	028763 archaeoglob	Q8a079 bacteroides			Q75m25 oryza sativ	8	Q6brl4 debaryomyce	Q7s4j9 neurospora	Q6ze35 oryza sativ		Q79wy2 streptococc		Q8pla2 streptococc
SOMMERS	ID	Q8R004	Q99K74	T100 HUMAN	Q9WVF1	Q6P153	AAH43802	QENUMO	AAH68408	Q9N4T2	Q9ZET7	Q9RLP6	YK67 YEAST	RFCL METMP	CAF29878	QBMMB8	VATC ASCSS	Q6XA <u>0</u> 9	AAP78735	028763	Q8A079	Q8U9Z7	Q7CSU1	Q75M25	AAS8832	Q6BRL4	Q7S4J9	Q6ZE35	BAC83465	Q79WY2	Q8K7T6	.Q8P1A2
	DB	:																			7	7	7	7	7	7	N	7	7	7	N	0
	Length	956	987	989	926	988	988	984	984	412	1438	5990	314	486	486	603	384	7191	7191	262	375	512	531	936	936	1351	37	99	99	218	218	н
	당성	1 6	7	7	6.4	ч	Н	ß	S	4	m	m	2	3	2	a	1.7		1.7	1.5	•	ä	ŗ.	ä	Η.	ä	÷	ö	ö	ö	6.0	•
æ	S &											m		m		М	m	m	m	m	m	•	m		m			m			m	m
	Score	173	173	173	169	109	109	9	66	61	S O	50	57	57	57	57	56.5	56.5	56.5	56	35.5	ഗ	ഗ	ഗ	m	55.5	ഗ	52	52	55	52	52
	Result No.	1	8	m	4	ហ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

09a051 streptococc 080uu4 mus musculu 009702 schrosacch 06my71 aspergillus 04fils candida gla 071eil bacillus 071eil bacillus 070eil bacillus 070eil bacillus 070eil bacillus 070eil bacillus 08c269 streptococc 097sx1 streptococc 073k1 wolbachia p Aasi4264 wolbachia 08ulb4 pyrococcus
09A051 09B0U4 NRD1_SCHPO 0SBY7] CAF32132 0SF018 07A121 AAQ08766 07VG3 Y175_STRR6 Y175_STRR6 Y175_STRR6 Q13HG1 AAS14264
<pre>000000000000000000000000000000000000</pre>
24700001114 1000001114 100000000000000000
8888881.3.4.6.000000000000000000000000000000000
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## ALIGNMENTS

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SOC	RN [2]  RC STRUTELES, and ISS;  RA Entinger M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  RA Eneson M., Gardon L., Bannett B., Johnson T.E., Sikela J.M.;  R. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  B. EMBL; AF483498; AAL90772.1;  DR RGD; MGI:1344385; Thrap4.  BR GO; GO:0000119; C:mediator complex; IDA.  GO; GO:0000166; P:transcription from Pol II promoter; IMP.  SEQUENCE 956 AA; 105941 MW; 41FC6F4D850D6540 CRC64;	Query Match 97.2%; Score 173; DB 2; Length 956; Best Local Similarity 100.0%; Pred. No. 9.7e-15; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 2 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 33 Db 664 YWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRS 695	RESULT 2  Q99K74  ID Q99K74  RC Q9K774  AC Q9K774  PRIJINIARY; PRI; 987 AA.  AC Q9K774  DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update)  DT 01-TMR-2004 (TrEMBLrel. 17, Last sequence update)  DT 01-MR-2004 (TrEMBLrel. 26, Last annotation update)  DB Thrap4 protein.  GN Name=Thrap4;  OS Mus musculus (Mouse).

```
EMBL, AF055995, AAC39855.1; -.
EMBL, D50920; BAA09479.2; ALT_INIT.
EMBL, AF27739; AAF78764.1; -.
EMBL, BC011375; AAH11375.1; -.
GGBLGW; HGNC:22963; THRAP4.
                      FROM N.A.
MEDLINE=22388257; PubMed=12477922;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Boxinse R.F., Jordan H.B., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Angak S.A., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley W., Solergren E.J., Lu X., Gibbs R.A.,
Racha J., Halton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Brakesley M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Chercation and initial analysis of more than 15,000 full-length human
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075448 Q4143; Q9NNYS;
075448 Q4143; Q9NNYS;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
01-07-2004 (Rel. 45, Last annotation update)
01-07-2004 (Rel. 45, Last annotation update)
17-broid hormone receptor associated protein complex 100 kDa component (Trapl00) (Thyroid hormone receptor associated protein 4) (Vitamin D3 receptor-interacting protein complex component DRIPl00) (Activator-recruited cofactor 100 kDa component) (RC100).
Name=THRAP4; Synonyms=TRAP100, DRIPl00, ARC100, KIAA0130;
HOMO sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yuan C.-X., Ito M., Fondell J.D., Fu Z.-Y., Roeder R.G.;
"The TRAP220 component of a thyroid hormone receptor-associated protein (TRAP) coactivator complex interacts directly with muclear receptors in a ligand-dependent fashion.";
Proc. Natl. Acad. Sci. U.S.A. 95:7939-7944(1998).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1344385; Thrap4.

GO; GO:0000113; C:mediator complex; IDA.

GO: GO:0006316; P:transcription from Pol II promoter; IMP.

SEQUENCE 987 AA; 109984 WW; 713C6A02C3C0B294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                       tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005409; AAH05409.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                SEQUENCE FROM N.A. STRAIN=mix FVB/N:
                                              MCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-EPA;

WEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETURNE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RIAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RIAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Haiseh F.,

Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Haiseh F.,

Braheton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,

Rhey J., Helton B., Ketteman M., Madan A., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhichguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberzation and initial analysis of more than 15,000 full-length human
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-!- TISSUE SPECIFICITY: Ubiquitous. Abundant in skeletal muscle, heart
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"Composite co-activator ARC mediates chromatin-directed
transacriptional activation.";
Nature 388:828-83(1999).
-i- FUNCTION: Plays a role in transcriptional coactivation. Plays a
role in nuclear hormone receptor-mediated transactivation.
-i- SUBUNIT: subunit of the large multiprotein complexes ARC/DRIP and
TRAP. Interacts and co-precipitates with Trap220. Does not
directly bind nuclear hormone receptors.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND IDENTIFICATION IN DRIP COMPLEX.
SEQUENCE FROM N.A., AND IDENTIFICATION IN DRIP COMPLEX.
MEDLINE=98301435; PubMed=9637681;

Rachez C., Suldan Z., Ward J., Chang C.-P.B., Burakov D.,

Erdjument-Bromage H., Tempst P., Freedman L.P.;

"A novel protein complex that interacts with the vitamin D3 receptor in a ligand-dependent manner and enhances VDR transactivation in a cell-free system.";

Genes Dev. 12:1787-1800(1998).
TISSUE=Bone marrow;
MEDLINE=5612530; PubMed=8590280;
MEDLINE=5612530; PubMed=8590280;
Magase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. IV. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by analysis of CDNA clones from human cell line KG-I.";
DNA Res. 2:167-174(1995).
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IDENTIFICATION IN ARC COMPLEX, AND SEQUENCE OF 1-11 AND 957-965.
MEDLINE=99249346; PubMed=10235267; DOI=10.1038/19789;
Nacaer A.M., Beaurang P.A., Zhou S., Abraham S., Solomon W.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUBS-EMERYO;

WEDLINES-2238827; PubMed=12477932;

Rausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

A Rianner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Robertein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcher B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rakealey B. W., Touchman J.W., Green E.D., Dickson M.C.,

Rakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rakealey M., Marka M.J.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                  Xenopus lacvis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC043802; AAH43802.1; -.
Interpro; IPR006162; Ppantne S. PROSTIE; PROSTIE; PROSTIE; PROSTIE; PROSPHOPAUETHEINE; UNKNOWN 1.
SEQUENCE 988 AA; 110513 MM; B780452FE568D3C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.2%; Score 109; DB 2; L
65.6%; Pred. No. 6.7e-06;
iive 3; Mismatches 8;
                                      PRT;
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MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.";
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                                      PRELIMINARY;
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Best Local Similarity
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Q6PI53;
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MEDLINE-9333122; pubmed=10406464;

Zhang J., Fondell J.D.;

"Identification of mouse TRAP100: a transcriptional coregulatory factor for thyroid hormone and vitamin D receptors.";

Mol. Endorimol. 13:1130-1140(1999).

EMBL, AF126543; AAD42776.1; -..

MOJ. MGI:1344385, Thrap4.

GO; GO:000019; C:mediator complex; IDA.

GO; GO:000019; P:transcription from Pol II promoter; IMP.
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204 A -> T (in Ref. 2).
555 E -> G (in Ref. 3).
110304 MW, CCEDETD4E74D890C CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOX-1994 (TrEMBLrel. 26, Last annotation update)
100 kpc thyroid hormone receptor associated protein.
Name-Thrap4; Synonyms-Trap100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          664 YWNLFPPKRPIKEVLTDIFAKVLEKGWVDSRS 695
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Best Local Similarity 96.9'
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Best Local Similarity luv...
Best Aca 32, Conservative
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989 AA;
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AAH43802;
02-MAR-2004 (TrEMELrel. 27, Created)
02-MAR-2004 (TrEMELrel. 27, Last sequence)
02-MAR-2004 (TrEMELrel. 27, Last ann
Thrap4-prov protein. RESULT 6 AAH43802 ID AAH4 AC AAH4 DT 02-M DT 02-M DT 02-M

Receptor

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MISDLINE=22388257; PubMed=12477932;

Atausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

A ptischul S.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

A ptachenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B atchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B connetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Saka S.A., McKennan K.J., Malan S.J., Gunarane P.H.,

A Richards S., Worley K.C., Hale S., Garcha A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A schiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A marra M.J.,

Marra M.J., Smailus of more than 15,000 full-length human and mouse contacts.
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                             Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Sträusberg R.;
Submir Eced (JAN-2203) to the EMBL/GenBank/DDBJ databases.
EMBL; ECOGOSC, AAH43802.1; -.
SEQUENCE 988 AA; 110513 MW; B780452FE568D3C6 CRC64;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
Brachydanio rerio (Zebrafish) (Danio rerio).
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MEDLINE=22341132; PubMed=12454917;
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                                                                            Xenopus.
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                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                               NCBI_TaxID=8355;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisleh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rahas S.S., Loquellano N.A., Petros G.J., Abramson R.D., Mullahy S.J., Roak S.A., McEwan P.J., Nckernan K.J., Malek J.A., Gunaratne P.H., R. Richards S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., Makesley R.W., Touchman J.W., Green B.D., Dickson M.C., Andrewski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., T. "Genezation and initial analysis of more than 15,000 full-length human
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Richards R.L., Feingold E.A., Magner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Scarsa M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., WcKernan R.J., Maraman P.H., WcKernan R.J., Maraman P.H.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,
Whiting M., Madan A., Young, A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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59.4%; Pred. No. 0.00016;
Minmalches 9; Indels
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Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO68408; AAH68408.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=22388257; PubMed=12477932;
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Best Local Similarity
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SEQUENCE FROM N.A.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 984;
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                                                                                                                                                                             Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2004);
Submitted (APR-4004)
Hypothetical protein.
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STRAINELISTON N2;
Lamar B., Le T.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE 984 AA; 110289 MW; 9567D437043F536D CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y50D4B.6.
ORFNames=Y50D4B.6;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99; DB 2; 1
Pred. No. 0.00016;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             691 YRNLLPARLPIRQALQSQFRKVLEKGWVDSHA 722
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STRAIN-Eristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 59.4 tes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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STRAIN=Bristol N2;
Waterston R.H.;
Submitted (MAR-2000) t
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Submitted (MAR-2000)
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Submitted (MAY-2002)
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Submitted (NOV-2002)
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STRAIN-Bristol N2;
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                 TISSUE=Embryo;
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Q9N4T2;
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A STATINGEN E.;

MISON R.;

MISON R.;

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AC066795; AR59493.2; ...

BRSSP; P11362; 1FGX.

WormPep; Y50D4B.6; CE56136.

OG GO:005524; F:AFT binding; IEA.

OG GO:0004413; F:AFT binding; IEA.

OG GO:0004413; F:AFT binding; IEA.

OG GO:000413; F:AFT binding; IEA.

CO; GO:0004113; F:ARSE Like.

INTER-PRO; IPR0011009; Kinase.like.

INTER-PRO; IPR0011009; Frot kinase.

INTER-PRO; IPR001109; Frot kinase.

INTER-PRO; IPR00109; PYT Dkinase.

INTER-PRO; IPR00109; PYT Dkinase.

PROMITS; PR00109; TYRKINASE.

PROSITE; PSC0011; PROTEIN KINASE DCM; 1.

PROSITE; PSC0011; PROTEIN KINASE DCM; 1.

PROSITE; PSC0011; PROTEIN KINASE DCM; 1.

PROSITE; PSC0011; PROTEIN KINASE DCM; 1.

PROSITE; PSC0011; RATHERNEN KINASE DCM; 1.

OR HYDOCHELICAL protein; Kinase; Transferase; Tyrosine-protein kinase.
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Billman-Jacobe H., McConville M., Haites R., Kovacevic S.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
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Mycobacterium smegmatis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
34.3%; Score 61; DB 2; Length 412,
Best Local Similarity 45.8%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 9; Indels
                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Peptide synthetase (Fragment).
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GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0048037; F:catalytic activity; IEA.

GO; GO:0048037; F:cofactor binding; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR010071; AA adenyl dom.

InterPro; IPR000873; AMP-bind.

InterPro; IPR001242; Condensatu.

InterPro; IPR001242; Condensatu.

InterPro; IPR001242; Condensatu.

Pfam; PF00510; PPbinding; I.

Pfam; PF00668; Condensation; 2.

Pfam; PF00650; PP-binding; 1.
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TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 WNLNPDKRPVFSECRDFFQKLLQQ 399
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                                                                   Waterston R.;
Submitted (NOV-2002)
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SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1772;
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01-MAY-1999 (
01-MAR-2004 (
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314 AA

PRT;

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MEDLINE=94262327; PubMed=8203164;
MEDLINE=94262327; PubMed=8203164;
Garcia-Cartelaejo J., Baladron V., Esteban P.F., Santos M.A., Bou G.,
Garcia-Cartelaejo J., Ballesta J.P.G., Jimenez A., del Rey F.;
Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Rey F.;
"The complete sequence of an 18,002 bp segment of Saccharomyces
cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 genes,
and six new open reading frames.";
Yeast 10:231-246(1994).
                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 44, Last annotation update)
Hypothetical 35.8 kDa protein in PRPIG-SRP40 intergenic region.
OrderedLocusNames=YKR087C; ORFNames=YKR407;
Saccharomyces cerevisiae (Baker, 8 yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycess;
Saccharomycetales; Saccharomycetaees;
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFCL METMP
                    RESULT 12
YK67_YEAST
ID _YK67_YEAST
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                                                                     P36163;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coppel R.L.;
"Identification of a peptide synthetase involved in the biosynthesis
"Identification of Mycobacterium smegmatis.";
Mol. Microbiol. 33:1244-1253(1999)
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterinees, Mycobacteriaceae, Mycobacterium.
                                                                                               ch 33.1%; Score 59; DB 2; Length 1438; 1. Similarity 52.4%; Pred. No. 78; 11; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5990;
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52.4%; Pred. No. 3.6e+02;
ive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PSSO075; ACP DOMAIN; 4.
PROSITE; PSO0061; ADH SHORT; UNKNOWN 1.
PROSITE; PSO0012; PADE SHORT; UNKNOWN 4.
PROSITE; PSO0112; PHOSPHOPANIETHEIRE; UNKNOWN 4.
SEQUENCE 5990 AA; 645938 WW; 25BAIC934EE90ZD5 CRC64;
                                                             1438 AA; 153614 MW; C90E52B84F2DA40E CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PSCOG455; AMP BINDING; 1.
PSCOCO12; PHOSPHOPANTETHEINE; UNKNOWN_1.
1438 1438
                                                                                                                                                                                                                                                                                                                 PRT; 5990 AA.
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GO; GO: 0048037; F: catalytic activity; IEA.
GO; GO: 0048037; F: cafactor binding; IEA.
GO; GO: 004815; F: metabolism; IEA.
InterPro; IPR01071; AA adenyl_dom.
InterPro; IPR01071; AA adenyl_dom.
InterPro; IPR010919; AMP-bind.
InterPro; IPR0101243; AMP-bind.
InterPro; IPR010160; NRPS synth.
InterPro; IPR010160; NRPS synth.
InterPro; IPR010161; Pp bind.
InterPro; IPR010161; Pp bind.
InterPro; IPR010161; Pp bind.
InterPro; IPR010161; Pp bind.
InterPro; IPR010161; AMPSINITNG.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01733; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRFAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRAMS; ITGR01743; AA-Adenyl-dom; A.
ITGRAMS; ITGR01743; AA-Adenyl-dom; A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99440174; PubMed=10510238;
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                                                                                                                                                                                                                                                                                                                                                                                                              Peptide synthetase
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                                          NON TER
SEQUENCE
        PROSITE;
PROSITE;
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Best Local
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Matches
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                                                                                                                                                                                                                      EMBL; 227116; CAA81638.1; -.
EMBL; 228312; CAA82166.1; -.
EMBL; 238312; CAA82166.1; -.
PIR, 538165; S38165.
GermChilne; 140066; -.
MENCPS; M48.018; -.
SGD; SC001795; YKR087C.
GO; GC:0005739; C:mitochondrial inner membrane; IDA.
GO; GC:0005739; C:mitochondrian; IDA.
GO; GC:0005739; C:mitochondrian; IDA.
GO; GC:0005739; C:mitochondrian; IDA.
GO; GC:0005739; P:metalloendopeptidase activity; IMP.
GO; GC:0005739; P:metalloendopeptidase activity; IMP.
GO; GC:0005135; Peptidase M48.
InterPro; IPR001915; Peptidase M48.
PFam; PF01435; Peptidase M48; I.
Hypothetical protein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2004 (Rel. 45, Created)
01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last semostation update)
Replication factor C large subunit (RFC large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22DD7EE3C747A440 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             large subunit).
Name=rfcL; Synonyms=rfcB; OrderedLocusNames=MMP0322;
Methanococcus maripaludis.
Archaea; Euryarchaeota; Methanococci; Methanococaeaes. Methanococcaeeaes.
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Potential.
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Gapa ..

6; Indels

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REPURDES FROW N.A.

WEDUINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-20196006; PubMed=10731132,

RAMADINE-2019606; PubMed=10731132,

RAMEND-10-2019606; PubMed=10731132,

RAMAN R.H., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAN R.H., Doyle C., Baxder E.G., Helt G., Nalson C.R., Gabor G.L.,

RAMAN R.H., Bould A., An H.J., Andrews-Feanharder D., Baldwin D.,

RAMAN R.H., Bould A., Barman B.P., Bhandari D., Belbhakov S.,

RAMADIN R.K., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Bould R., Gorrell J.H., Gu Z., Guan P., Harris M., Harvel D., Hender D., Hernandez J.R., Houck J., Bould R., Month R., Houston R., Houston R., Houston R., Houston R., Houston R., Mattel B., McInton R., Morleson D., Morleson D., Morleson D., Morleson D., Morleson D., Morleson D., Morleson D., Morleson R., Mount S.M., Mollon R., Mollon R., Wolden R., Wang R., Sun B., Pollator R., Wang R., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun B., Sun
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                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endoptery, Endoptery, Endoptery, Ephydroidea, Endoptery, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                              603 AA
  4; Mismatches
                                                                                                                                                                                                                                              PRT;
                                                                                                       446 PPKEPLKEVIEETLEKSVEK 465
                                                      7 PPKRPIKEVLTDIFAKVLEK 26
  10; Conservative
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     Matches
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QBMMB8
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstainnthe between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                            "Complete genome sequence of the mesophilic hydrogenotrophic methanococcus maripaludis.",
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Part of the RFC dlamp loader complex which loads the PCNA sliding clamp onto DNA (By similarity).
-!- SUBUNIT: Heterowultimer composed of small subunits (rfcs) and large subunits (rfcL) (By similarity).
-!- SIMILARITY: Belongs to the activator I small subunits family. RfcL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.E., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T., Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G., Saenphimmachak C., Soell D., Whitman W.B., Larimer F.W., Olson M.V.,
                                                                          STRAIN=S2 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.E., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T., Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G., Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 32.0%; Score 57; DB 1; Length 486; Local Similarity 50.0%; Pred. No. 45; Los 10; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.0%; Score 57; DB 2; Length 486; 50.0%; Pred. No. 45;
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BX957219; CAF29878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaecta; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
NCBI TaxID=39152;
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Last annotation update)
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03-NAR-2004 (TrEMBLrel. 27, Last sec
04-NAY-2004 (TrEMBLrel. 27, Last an
Replication factor C, large subunit.
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Best Local Similarity
                                                   SEQUENCE FROM N.A.
NCBI_TaxID=39152;
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                                                                                                                                                                                                                                              Leigh J.A.;
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

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MEDINE=22456070; PubMed=12537573; Kaninler B., Carlson J., Svirskas R., Kaninker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R., Astburner B., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M., Astburner M., Celniker S.E.;

"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.", Genome Biol. 3:RESEARCH0084(2002).
                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
MAISTA S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mista S., Crosby M.A., Mungall C.J., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
32.0%; Score 57; DB 2; Length 603;
Best Local Similarity 35.1%; Pred. No. 57;
Matches 13; Conservative 6; Mismatches 10; Indels
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Search completed: November 10, 2004, 12:27:15 Job time : 39.1065 secs

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Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence

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Sequence 20024, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PEPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.6%; Score 44; DB 4; Length 175; llarity 53.8%; Pred. No. 16; Conservative 2; Mismatches 4; Indels
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US-08-489-0538-7646
US-08-190-139A-7646
US-08-190-139A-7646
US-08-190-139A-7646
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US-08-911-321-11
Sequence 11, Application US/08911321
Fatent No. 6010703
GENERAL INFORMATION:
APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Poxvirus
TITLE OF INVENTION: Peline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: 12
CORRESPONDENCES: 12
STREET: 2190 Commons Parkway
CITY: Okemos
STREET: Alchigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20024
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US-09-252-991A-20024
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39, Appl
38, Appl
40, Appl
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                                                                                   '; Search time 5.65895 Seconds (without alignments) 222.664 Million cell updates/sec
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Sequence 40,
Sequence 42,
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-504-67-3

US-08-504-67-3

US-09-252-91A-23110

US-09-252-91A-23110

US-09-252-91A-23310

US-09-252-91A-23910

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US-09-148-656-135

US-09-252-91A-30913

US-09-252-91A-30913

US-08-311-71A-112

US-09-147-6568

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US-08-147-46-39

US-08-147-47-346-40
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Maximum Match 100%
Listing first 45 summaries
                                                         protein search, using sw model
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1 LFTILLTLWTMRCSSTPSG 19
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels
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GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: MoDonell, Michael W.
TITLE OF INVENTION: Recombinant Feline Herpes virus
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSERE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
COMPUTER: IBM 330 466 DX2
COMPUTER: IBM 330 466 DX2
SOFTWARS: PATENT: PC-DOS/MS-DOS
SOFTWARS: PATENT: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13975
FILING DATE: 26-OCT-1995
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/329,883
FILING DATE: 26-OCT-1994
CLASSIFICATION:
NAME: White: John P:
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 33118-PCT
TELECOMONICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TREET: 1185 Avenue of the Americas CITY: New York STARTE: New York COUNTRY: USA
APPLICATION NUMBER: US/08/504,617
ETLING DATE:
CLASSIPLICATION: 435
PRIOR APPLICATION: 435
FRIING DATE: MARCH 22, 1994
ATTIONO DATE: MARCH 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: GOTHLEY, MAY E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 258-520
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
FRATURE: protein
FRATURE: protein
        US/08/504,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /label= ORF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein
PCT-US95-13975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 WTSRCINTPS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 WIMRCSSTPS 18
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Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels
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Retent No. 6521236

GENERAL INFORMATION:
APPLICANT: Willemes, Martha Jacoba
APPLICANT: Sondermeijer, Paulus Jacobus Antonius
APPLICANT: Sondermeijer, Paulus Jacobus Antonius
APPLICANT: Sondermeijer, Paulus Jacobus Antonius
TITLE OF INVENTION: Vector vaccines of recombinant
TITLE OF INVENTION: Feline herpesviruses
NUMBARCE ADDRESS:
ADDRESSER: Akzo No. 6521236e1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
              MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/096,183
FILING DATE: UJLY 26, 1993
ATTOMEN'AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REGISTRATION NUMBER: 20,931
REGISTRATION INFORMATION:
TELEPHONE: (517) 347-4103
TELEPA: No. 610703e
INFORMATION FOR SEQ ID NO: 11:
SEMPRATION FOR SEQ ID NO: 11:
SEMPRATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
DENTIFICATION METHOD: Deduced Sequence
OTHER INFORMATION: GE
US-08-911-321-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Akzo No. 6521236el
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
CUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Feline herpesvirus-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGI. --
MOLECULE TYPE:
DESCRIPTION: Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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290 WTSRCINTPS 299
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US-08-504-617-3
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANN.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107166-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 26505
LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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18;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PZ001P1
CURRENT APPLICATION NUMBER: US/09/148,545
                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFILING DATE: 1997-03-07
REPLING DATE: 1997-03-07
REPLING DATE: 1997-03-07
REPLING DATE: 1997-03-07
REPLING DATE: 1997-03-07
REPLING DATE: 1997-03-07
REPLING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-23
APPLICATION UNDRER: 60/047,597
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/047,583
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Sequence 135, Application US/09148545
Patent No. 6590075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LFTILLTLWIMRCSSTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-26505
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                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITHE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITHE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITE OF INVENTION: ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 107196.136
CURRENT PELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23110
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 1996-0347
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31682
LENGTH: 183
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                                                           Gaps
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       Query Match 43.6%; Score 44; DB 5; Length 532; Best Local Similarity 70.0%; Pred. No. 54; Matches 7; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 4; Length 183;
Pred. No. 25;
1; Mismatches 5; Indels
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Patent No. 6747137;
GENERAL INFORMATION: APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                         US-09-252-991A-23710
; Sequence 23710, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-270-767-31682
US-09-270-67-31682, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Drosophila melanogaster
US-09-270-767-31682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%;
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ilarity 53.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.0
Matches 7; Conservative
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                                                                                                                                 290 WTSRCINTPS 299
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                                                                                                   9 WIMRCSSIPS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-248-796A-26505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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MUMBER: 60/047,581 1997-05-23 1997-05-23 NUMBER: 60/047,500 1997-05-23 NUMBER: 60/047,500 1997-05-23 NUMBER: 60/047,591 1997-05-23 NUMBER: 60/047,693 NUMBER: 60/047,698	1997-05-23 1997-05-23 1997-05-23 NUMBER: 60/047, 1997-05-23 NUMBER: 60/047, 1997-05-23 NUMBER: 60/043, 1997-05-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11 NUMBER: 60/043, 1997-04-11	NUMBER: 60/043,197 1997-04-11 1997-04-11 1997-04-11 1997-06-06 1997-08-26 1997-08-26 1997-08-26 1997-08-26 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-27 1997-08-28 1997-08-28 1997-08-28 1997-08-28 1997-08-28 1997-08-28 1997-08-28 1997-08-28
PPLICATION LLING DATE PPLICATION LLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE ILLING DATE ILLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE PPLICATION ILLING DATE	LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.  PLICATION LING DATE.	TILING DATES  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELICATION  PELI
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EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 899
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 894
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 814
EARLIER APPLICATION NUMBER: 60/056, 814
EARLIER APPLICATION NUMBER: 60/056, 814
EARLIER APPLICATION NUMBER: 60/056, 814
EARLIER APPLICATION NUMBER: 60/056, 815
EARLIER APPLICATION NUMBER: 60/056, 815
EARLIER APPLICATION NUMBER: 60/056, 815
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-23
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EARLIER PRILING DATE: 1997-06-22
EARLIER PRILING DATE: 1997

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Sequence 30911, Application US/09252991A

Sequence 30911, Application US/09252991A

Sequence 30911, Application US/09252991A

APPLICANT: MAXC J. Rubenfield et al.

APPLICANT: MAXC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PELING DATE: 1999-02-18

PRIOR PELING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30911

LENGTH: 436
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Pred. No. 92;
2; Mismatches 0; Indels
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     1; Indels
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APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
LENGTH: 116
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41.1%; Score 41.5; D
Best Local Similarity 50.0%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5265, Application US/09621976 Patent No. 6639063 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 112, Application US/08311731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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       7; Conservative
                                                  10 TWRCSSTPSG 19
                                                                                   41 SMRCASTPPG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LTLWTMRC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: -21..-1
US-09-621-976-5265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SIGNAL
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       Matches
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Sequence 32999, Application US/09252991A

Sequence 32999, Application US/09252991A

Sequence 32999, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINGA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 248

LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27913, Application US/09252991A

Sequence 27823, Application US/09252991A

Sequence 27823, Application US/09252991A

GENERAL INFORMATION:
APPLICANT:
MAC D. Rubenfield et al.
APPLICANT:
MAC D. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27823

LENGTH: 229
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Pred. No. 44;
1; Mismatches 1; Indels
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41.6%; Score 42; DB 4; Length 229;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 2; Indels
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER PILING DATE: 1997-08-22
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SEQ ID NO 135
; LENGTH: 222
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 77.8%;
Matches 7; Conservative
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                142 LDLWTVRCS 150
                                                                                                                                                                                                                                                                                                                     6 LTLWTMRCS 14
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Best Local Similarity
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US-09-252-991A-27823
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Sequence 30903, Application US/09252991A

Patent No. 651795

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General No. 67170

General No. 67170

General No. 67170

General No. 67170

General No. 
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIANNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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Best Local Similarity 32.0%; Pred. No. 65;
Matches 8; Conservative 5; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/720-3500
TELEFAX: 617/720-341
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DENGTH: 266 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       BOSTON
3: MASSACHUSETTS
TRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: MYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-252-991A-30903
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Query Match
40.6%; Score 41; DB 4;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches ;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION UNMER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER PILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/047,615
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                               Sequence 568, Application US/09149476
Patent No. 6420526
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-03-07
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                                                                                                    9 WIMRCSSIPS 18
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R FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047, 632

RR FILING DATE: 1997-05-23

RR FILING DATE: 1997-06-23

RR FILING DATE: 1997-06-23

RR FILING DATE: 1997-04-11

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RR FILING DATE: 1997-04-11

RR FILING DATE: 1997-04-11

RR FILING DATE: 1997-04-11

RR FILING DATE: 1997-06-60

RR APPLICATION NUMBER: 60/043,673

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,899

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,899

RR RELING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,892

RR RILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,892

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RR APPLICATION NUMBER: 60/056,892

RR RILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,892

RR RILING DATE: 1997-08-22

RR RILING DATE: 1997-08
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RR APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631
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APPLICATION NUMBER: 60/056,911
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,612
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BARLIER BEARLIER 
Gaps ö 40.6%; Score 41; DB 4; Length 251; 53.8%; Pred. No. 73; tive 3; Mismatches 3; Indels EARLIER APPLICATION UNDER 60/056,845
EARLIER APPLICATION UNDER 60/056,845
EARLIER APPLICATION UNDER 60/056,892
EARLIER APPLICATION NUMBER 60/056,892
EARLIER APPLICATION NUMBER 60/047,595
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EARLIER APPLICATION NUMBER 60/056,676
EARLIER APPLICATION NUMBER 60/056,6 EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 Query Match
Best Local Similarity 53.8
Matches 7; Conservative

193 IMSLWTQSHSSTP 205 S LLTLWIMRCSSTP 17

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Search completed: November 10, 2004, 12:32:30 Job time : 6.65895 secs

Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database :

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      Sequence
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Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpini, Julia
APPLICANT: Alpini, Julia
APPLICANT: Alpini, Julia
APPLICANT: Alpini, Julia
APPLICANT: Alpini, Julia
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR PRING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 19
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6 US-10-437-963-166688

0 US-09-934-070-8

US-10-924-070-8

US-10-424-599-152966

5 US-10-424-599-152966

7 US-10-425-115-236845-7

7 US-10-425-115-236845-7

7 US-10-425-115-318411-7

7 US-10-425-115-318412-7

7 US-10-425-115-318412-7

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7 US-10-425-115-318282-7

7 US-10-425-115-29759-7

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100.0%; Score 101; DB 14;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-425-115-240916
; Sequence 240916, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LFTILLTLWTMRCSSTPSG 19
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      TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Appl
Sequence 240916,
                                                                                                                                November 10, 2004, 15:53:52; Search time 18.3256 Seconds (without alignments) 366.225 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-042-115-240916
US-10-0424-599-198283
US-10-163-198-25
US-10-163-198-25
US-10-156-761-10847
US-10-156-761-10847
US-10-437-963-115917
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                              US-10-092-750-17
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1 LFTILLTLWTMRCSSTPSG 19
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Gaps

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264596765432

Result

Gaps

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Sequence 25, Application US/10163198

Sequence 25, Application US/10163198

Publication No. US20030126645A1

GENERAL INFORMATION:

APPLICANT: Rebeca E. Cahoon

APPLICANT: Elmer P. Heppard

APPLICANT: Elmer P. Heppard

APPLICANT: Hajime Sakai

ITLE OF INVENTION: Alteration Of Embryo/Endosperm Size During Seed Development

FILE REFERENCE: BB1487 US NA

CURRENT FILING DATE: 2002-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 111

SEQ ID NO 25

LENGTH: 542
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                                                                                                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_21074C.1.pep
US-10-424-599-198283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 251, Application US/10231417
Publication No US20030176681A1
GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 148 Human Secreted Proteins
FILE REPRENCE: PZ0191
CURRENT APPLICATION NUMBER: US/10/231,417
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US/09/296,622
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 619
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 251
LINGTH: 116
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47.0%; Score 47.5; D
Best Local Similarity 50.0%; Pred. No. 55;
Matches 11; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LFTILLTLW---TWRCSSTPSG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 LLTIMVTLWLSMTFFCWSHPGG 47
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SEQ ID NO 198283
LENGTH: 242
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Glycine max
US-10-163-198-25
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 11; Conserva
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US-10-231-417-251
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APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
ILLE REFERENCE: DEX-0283
CURRENT APPLICANTON: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0283
CURRENT APPLICATION NUMBER: US/10/001,870
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR FILING DATE: 2000-11-21
us-10-C

APPLICANT: La Rosa, Thomas J.

APPLICANT: Acvalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REPRESENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 240916

LENGTH: 151

TYPF.
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
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Pred. No. 7.5;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_151294C.1.pep
US-10-425-115-240916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 184, Application US/10001870; Publication No. US20020150924A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LFTILLTLWIMRCSSTPSG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.5%;
66.7%;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 184
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 LWALRCRSSPSG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LWTMRCSSTPSG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (62)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (70)
LOCATION: (70)
LOCATION: (70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-08-764-891-3368
                                                                                                                                                                                                                                   Sequence 3368, Application US/09764891
; Sequence 3368, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TILE REFERENCE: PC006
; CURRENT REPLICANTION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 2; Indels
61.5%; Pred. No. 29;
tive 1; Mismatches
                                                                         5 LLTLWTMRCSSTP 17
                                                                                                                     47 LISRWISRCSCTP 59
Best Local Similarity 61.5
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                 RESULT 9
US-09-764-891-3368
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Best Local Similarity 57.1%; Pred. No. 67;
Matches 8; Conservative 2; Mismatches 4; Indels
                                                                                                   Query Match

46.5%; Score 47; DB 14; Length 116;
Best Local Similarity 52.4%; Pred. No. 32;
Matches 11; Conservative 4; Mismatches 4; Indels
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals stop translation
US-10-231-417-251
                                                                                                                                                                                                                                                                                                                                           WESCULIO
Sequence 10847, Application US/10156761
Sequence 10847, Application US/10156761
GENERAL INPORMATION:
APPLICANT: OWURA, SATOCKI
APPLICANT: ISEDA, HAROO
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIRA, TANN
APPLICANT: SHIRA, TANN
APPLICANT: SHIRA, TANNOSHI
APPLICANT: SHIRA, TANNOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEGOID NO 10847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10847
                                                                                                                                                                                                      1 LFT -- ILLILIWIMRCSSTPSG 19
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56 LFTGPLLTTHHLLCETSPSG 76
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235 VTLWTRRTAHTPGG 248
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Gequence 121796, Application US/10437963

j Sequence 121796, Application US/10437963

j Publication No. US20040123343A1

general information:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: APPLICANT: APPLICANT: APPLICANT: Boukharov, Andrey A.
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Li, Ping
 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Brade
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 121796
 LENGTH: 98 ; FEATURE: ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_24786C.1.pep US-10-437-963-121796

US-10-425-115-213984

US-10-425-115-213984, Application US/10425115

Sequence 213984, Application No. US20040214272A1

Sequence 213984, Application No. US20040214272A1

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)

CURRENT FILING DAIE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 213984

Length 73;

45.5%; Score 46; DB 17;

Query Match

; OTHER INFORMATION: Clone ID: MRT4577\_12674C.1.pep US-10-425-115-213984

TYPE: PRT ORGANISM: Zea mays FEATURE: OTHER INFORMATION:

; 0

Gaps

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TILE OF INVENTION: Brad

TILLS OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE PEPRENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NOS: 204966
SEQ ID NO 166688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barbazuk, Brad Applicant: Applicant: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Riants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREMENT: 38-21 (53221)B
CURRENT APPLICATION VIMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 127870
LENGTH: 84
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Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 5; Indels
                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_30279C.1.pep
US-10-437-963-127870
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       Best Local Similarity 43.8%; Pred. No. 31;
Matches 7; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Sequence 127870, Application US/10437963
Publication No..US20040123343A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                   1 LFTILLTLWIMRCSST 16
                                                                                                                                                             38 LASVILAIFTVRCTST 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LFTILLTLWTWRCSS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Publication No. US2004012334341

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Acvalic, David K.

APPLICANT: Acvalic, David K.

APPLICANT: Acvalic, David K.

APPLICANT: Application Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Brants and Uses Thereof for Plant Improvement

FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 36-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 115917

ENGURI 1478
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Publication No. US20040031072A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: About Yihua
APPLICANT: Cao Yong Yihua
APPLICANT: Cao Yong Yihua
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Query Match
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.6%; Score 45; DB 15; Length 55;
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US-10-424-599-181785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_19469C.1.pep
US-10-437-963-115917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(1478)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                             4 ILLTLWIMMRCSSTPSG 19
                                                                                                                                                                                           64 VVVESWTMESSSLPSG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TLWTMRCSSTPSG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                    US-10-437-963-115917
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Query Match

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us-10-092-750-17.rapb
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  Gaps
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US-09-934-070-8

i Sequence B, Application US/09934070

j Sequence B, Application No. US2003002004A1

j GENERAL INFORMATION:
 j APPLICANT: Lipton, Stuart A.
 j APPLICANT: Lipton, Stuart A.
 j APPLICANT: Chatcerton, Jon E.
 j APPLICANT: Chatcerton, Jon E.
 j APPLICANT: Chatcerton, Jon E.
 j APPLICANT: APPLICANT: EXCITATORY GLYCINE RECEPTORS AND METHODS
 j TITLE OF INVENTION: EXCITATORY GLYCINE RECEPTORS AND METHODS
 j TITLE OF INVENTION NUMBER: US/09/934,070
 j CURRENT FILING DATE: 2001-08-20
 j CURRENT FILING DATE: 2001-08-20
 j SEQ ID NO 8
 j EBNGTH: 1005
 j LENGTH: 1005
 j LENGTH: 1005
 j TYPE: PRT
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Best Local Similarity 61.5%; Pred. No. 5.18+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0
7; Indels
4; Mismatches
                                   5 LLTLWTWRCSSTP 17
8; Conservative
Matches
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Search completed: November 10, 2004, 16:36:01 Job time : 19.3256 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

November 10, 2004, 11:36:51 ; Search time 3.84105 Seconds (without alignments) 475.942 Million cell updates/sec

US-10-092-750-17

101 1 LFTILLTLWTMRCSSTPSG 19 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | probable exported | ਯ      | w      | hypothetical prote | w      | ical prot | _      | ซ      | _      | _      | _      | hypothetical prote | glutamyl-tRNA amid | glutamyl-tRNA amid | hypothetical prote | stromal cell-deriv | tra    | probable transcrip | cal    | lpsA protein [impo | acetyl-CoA carboxy | GTP-binding regula | protein R04B3.3 [i | pre-T-cell recepto | probable membrane | GTP-binding regula | oinding 1 | -      | oinding regul |
|-----------|----------------|-------------------|--------|--------|--------------------|--------|-----------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-----------|--------|---------------|
| SUMMARIES | Ω              | AD0357            | D82441 | AH0577 | T15432             | E65083 | QXBP6L    | T16950 | A34413 | T42312 | T12798 | S74540 | E72566             | B97724             | E71725             | H84698             | JC7587             | G90667 | C85518             | H83973 | AH3417             | T02750             | 829121             | C89481             | A55169             | AI0713            | RGBOB2             | RGBOB1    | RGFFBH | RGHUB1        |
|           | DB             | 7                 | N      | 7      | N                  | ~      | Н         | ~      | ~      | ~      | N      | ~      | N                  | ~                  | ~                  | ~                  | N                  | 7      | N                  | 7      | N                  | 7                  | Ņ                  | (7                 | ч                  | ~                 |                    | -1        | н      | -             |
|           | Length         | ıω                | v      | 255    | φ                  | φ      | 57        | 119    | m      | Φ      | 4      | σ      | 0                  | σ                  | 493                | Н                  | N                  | Φ      | σ                  | 0      | N                  | œ                  | N                  | æ                  | 0                  | ~                 | N                  | 4         | 4      | 4             |
|           | Query<br>Match |                   | 45.5   | 45.0   | 4.                 | •      | ۳,        | 43.6   | •      | 'n     | 'n     | 'n     | 'n                 | 'n                 | 42.6               | ä                  | ä                  | ä      |                    | ä      | ä                  | ä                  | ö                  |                    | 0                  |                   | 。                  | 。         | 40.6   |               |
|           | Score          | 4                 | 4      | 45.5   | 45                 | 45     | 44        | 44     | 44     | 43     | 43     | 43     | 43                 | 43                 | 43                 | 43                 | 42                 | 42     | 42                 | 42     | 42                 | 42                 | 41                 | 41                 | 41                 | 41                |                    | 41        | 41     | 41            |
|           | Result<br>No.  | п                 | 7      | ო      | 4                  | w      | 9         | 7      | ω      | თ      | 10     | 11     | 12                 | 13                 | 14                 | 15                 | 16                 | 17     | 18                 | 19     | 20                 | 21                 | 22                 | 23                 | 24                 | 25                | 56                 | 27        | 28     | 29            |

|                    | ALIGNMENTS |    |     |      | 3    | ś        |
|--------------------|------------|----|-----|------|------|----------|
| hypothetical prote | T30966     | 71 | 503 | 40.6 | 41   | ın.      |
| ribonuclease inhib | A31857     | N  | 456 | 40.6 | 41   | 4.       |
| G-protein beta cha | T07376     | N  | 377 | 40.6 | 41   | m        |
| GTP-binding protei | T04089     | N  | 377 | 40.6 | 41   | C)       |
| GTP binding protei | T04086     | C) | 377 | 40.6 | 41   | Ξ,       |
| GTP-binding protei | T16985     | ~  | 377 | 40.6 | 41   | <u>o</u> |
| GTP-binding protei | T03256     | N  | 375 | 40.6 | 41   | . 68     |
| GTP-binding regula | S34348     | N  | 341 | 40.6 | 41   | œ        |
| GTP-binding regula | RGOOBE     | н  | 341 | 40.6 | 41   | .7       |
| G-protein beta-sub | 153871     | N  | 340 | 40.6 | 41   | 9        |
| G protein beta 1 - | JC5057     | N  | 340 | 40.6 | 41   | Š        |
| hypothetical prote | T20830     | 0  | 340 | 40.6 | 41   | 34       |
| GTP-binding regula | RGMSB4     | Н  | 340 | 40.6 | 41   | ũ        |
| GTP-binding regula | RGKWB      | -  | 340 | 40.6 | . 41 | 2        |
| GTP-binding regula | RGHUB3     | н  | 340 | 40.6 | 41   | ᅼ        |
| GTP-binding regula | RGHUB2     | Н  | 340 | 40.6 | 41   | 0        |

|      |     | 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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|      |     | 20000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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Probable exported protein YPO2935 [imported] - Yersinia pestis (strain CO92)
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: O2-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004
C.Accession: AD0357
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Frentice, M.B., deno-rarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; id., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F. Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Accession: AD0357
A; Stetus: preliminary
A; Stetus: preliminary
A; Residues: 1-186 <KUR>
A; Cross-references: UNIPROT:Q8ZCP2; GB:AL590842; PIDN:CAC92183.1; PID:g15980896; GSPDB:GA
G; Genetics:
A; Genetics:

Gaps ö Query Match
45.5%; Score 46; DB 2; Length 186;
Best Local Similarity 60.0%; Pred. No. 8.9;
Matches 9; Conservative 3; Mismatches 3; Indels

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1 LFTILLTLWIMRCSS 15

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22 LFLVLVTLLTIACSS 36 임

Conserved hypothetical protein VCA0581 [imported] - Vibrio cholerae (strain N16961 serogy conserved hypothetical protein VCA0581 [imported] - Vibrio cholerae (strain N16961 serogy C; Species: Vibrio cholerae (c) Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004 C; Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004 C; Aug-2000 #text\_change 09-Jul-2004 C; Aug-2000 #text\_change 09-Jul-2004 C; Aug-2000 #text\_change 09-Jul-2004 C; Aug-2000 #text\_change 09-Jul-2004 C; Fraser, C.M.

Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Accession: D82441 A; Status: preliminary A; Status: preliminary A; Status: preliminary A; Status: preliminary A; Status: preliminary A; Status: D23 4HEL> A; Cross-references: UNIPROT:Q9KM08; GB:AE004389; GB:AE003853; NID:g9657989; PIDN:AAF9648: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Map position: 2

Query Match

45.5%; Score 46; DB 2; Length 263;

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C,Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C,Accession: E65083
R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUD:97426617; PMID:9278503
A,Accession: E65083
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Nolecule type: DNA
A,Residues: 1-560 *BLAT>
                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q46839; GB:AE000380; GB:U00096; NID:g1789344; PIDN:AAC76011.1
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: L-lactate permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: Q10026, EMBL: U28738; NID: 9861262; PID: 9861266; PIDN: AAA68311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-9, C',11-57 <SAN>
A;Cross-references: GB:U02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:G215104;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein A-57 (nin region) - phage lambda
C.Species: phage lambda
C.Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C.Accession: B43011; G43016; A04392
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C;Superfamily: phage lambda hypothetical 7K protein (nin region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Daniels, D. sebaniels Acid Sequence Database, September 1982 A.Reference number: A94614
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%; Pred. No. 32;
Matches 6; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues; 1-57 < ADAN-
A; Cross-references: UNIPROT: P03767
A; Cross-references: UNIPROT: P03767
B; Sanger, F; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen,
J. Mol. Biol. 162, 729-773, 1982
A; Title: Nucleotide sequence of bacteriophage lambda DNA.
A; Reference number: A92891; MUID:83189071; PMID:6221115
A; Accession: G43016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rifulton, L. submitted to the EMBL Data Library, June 1995
A, Description: The sequence of C. elegans cosmid T28D9.
A, Reference number: Z18614
A, Accession: T16950
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-119 < FUL.>
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Pred. No. 6.5;
2; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                         molydopterin-containing oxidoreductase membrane anchor chain STY0661 [imported] - Salmc SSpecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0577
R;Parkhill, J: Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H.T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Ouail, M.; Rutherford, F.; Pindiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:P52484; EMBL:U39674; NID:g1049421; PID:g1049424; PIDN:AAA804
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1959 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1959 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15432
A;Reference number: Z18349
A;Reference number: Z18349
A;Reterence number: Z18349
A;Reterence number: Z18349
A;Reterence number: Z18349
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E65083
Putative L-lactate permease - Escherichia coli (strain K-12)
C;Species: Escherichia coli
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C;Superfamily: probable dimethylsulfoxide reductase chain C
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Molecule type: DNA
Residues: 1-260 <FAV>
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A;Residues: 1-260 <FAV>
A;Cros: references: UNIPROT:P52484; EMBL:U39674; NI
C;Genetics:
A;Gene: CESP:C06E2.3
A;Introns: S4/3; 129/2; 171/3
C;Superfamily: yeast ubiquitin-protein ligase UBC1
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Pred. No. 17;
2; Mismatches
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                                                       Mismatches
                             Pred. No. 5; Mismatc
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134 FTMLLFFITVWVMGCAAIP 152
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                                                                                                               3 TILLTLWTMRCSSTPSG 19
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Best Local Similarity 55.6%;
Matches 10; Conservative
                             llarity 47.1%;
Conservative
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| TLLMTLGLAACSASPTG
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A;Molecule type: DNA
A;Residues: 1-255 <PAR>
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Matches 9; Conserv
                                Best Local Similarity
Matches 8; Conserv
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A, Accession: T12796
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A, Residues: 1-148 cLaz.
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A, Residues: 1-148 cLaz.
A, Residues: 1-148 cLaz.
A, Residues: 1-148 cLaz.
A, Excullate, S.; Bruschi, C.V.; Caddwell, B.; Capuano, V.; Carer, N. M.; Choi S, Errington, V.; Garer, N. M.; Choi A, Enrington, V.; Bront, S.; Bront, S.; Bront, S.; Bruschi, C.V.; Caddwell, B.; Capuano, V.; Carer, N. M.; Choi A, Enrington, V.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A, Enrich, S.D.; Emmerson, P. T.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A.; Harbore: Poulger, D.; Firitz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A.; Harwood, C.R.; Henauc, A.; Hilbert, H.; Holsappel, S.; Hullo, M.F.; Kochter, P.; Koningertein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidue, A.; Hardinois, A.; Laudhors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Maucel, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Tosaro, T.; Schoreter, R.; Schore, B.; Rock, M.; Sadich, J.; Sckowska, A.; Schroeter, R.; Schoffone, P.; Sekiguchi, J.; Sckowska, A.; Schroeter, R.; Schoffone, P.; Sekiguchi, J.; Sckowska, A.; Vanamac, P.; Hille: The complere genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reterance number: A69580; MUID:9004033; PMID:9344777
A; Accession: C69911
A; Rocesion: C69011
A; Rocesion: C69011
A; Rocesion: C69011
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-230 «KAN»
A,Cross-references: UNIPROT:P72685; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA1669;
A,Cross-references: UNIPROT:P72685; EMBL:D90899; GB:AB001339; NID:g1651650
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C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 874540
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
D, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A.Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophaga. A.Reference number: 217583
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42.6%; Score 43; DB
Best Local Similarity 41.2%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches
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nes 7; Conserva
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E72566
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Reses: 1-432 <SOS>
A; Cross-references: UNIPROT: P15287; GB: J05059; NID: g155709; PIDN: AAA27741.1; PID: g155716
C; Superfamily: California sea hare atrial gland granule-specific antigen
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hypothetical protein - phage SPP1
c;beciss; phage SPP1
c;beciss phage SPP1
c;becission: T42312
c;baccession: T42312
c;Accession: T42312
d;Accession: Table Complete nucleotide sequence and functional organization of Bacillus subtil
d;Reference number: Z22137; MUID:98094274; PMID:9434185
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C;Species: Aplysia californica (California sea hare)
C;Daccesion: A34413
R;Sossin, W.S.; Kreiner T.; Barinaga, M.; Schilling, J.; Scheller, R.H.
J. Biol. Chem. 264, 16931-16940, 1993
A;Title: A dense core vesicle protein is restricted to the cortex of granules in the A;Reference number: A34413; MUID:89380331; PMID:2777814
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C;Species: Bacillus subtilis phage SPBc2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12798; C69911
S;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
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                                                                                                                                                                                           Score 44; DB 2; Length 119;
Pred, No. 12;
0; Mismatches 3; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <ALO>
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Pred. No. 37;
0; Mismatches
                      A, Experimental source: strain Bristol N2 (Squetics: 25, Genetics: A, Gene: CESP 128D9.9
A) Introns: 32/1
                                                                                                                                                                                                  43.6%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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LFTIVVTVWT 57
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Search completed: November 10, 2004, 12:29:21
Job time : 4.84105 secs
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A, Molecule type: DNA
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hypothetical protein APE1815 - Aeropyrum pernix (strain K1)
C.Species: Aeropyrum pernix
C.Species: Aeropyrum pernix
C.Jaccesion: E72566
Accession: E72566
Askavarabayasi, Y.; Hinn, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K)
DNA Res. 6, 83-101, 1999
A.Stitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-301 <KAM>
A;Cross-references: UNIPROT:09YAY0; DDBJ:AP000062; NID:g5105244; PIDN:BAA80818.1; PID:d1
A;Experimental source: strain K1
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Andecule type: DNA
A;Residues: 1-493 «KUR»
A;Cross_references: UNIPROT:Q92J75; GB:AE006914; PIDN:AAL02732.1; PID:g15619244; GSPDB:G
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-NOv-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: B71725
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature: 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9828893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: B97724
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97724
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C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: Aeropyrum pernix hypothetical protein APE1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
42.6%; Score 43; DB 2;
Best Local Similarity 42.9%; Pred. No. 39;
Matches 6; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.6%; Score 43; DB
47.4%; Pred. No. 59;
tive 4; Mismatches
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184 LMLTWSLGCTSTPA 197
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Matches 9; Conserv
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hypothetical protein At2g29650 [imported] - Arabidopsis thaliana
(C)Species: Arabidopsis thaliana (mouse-ear cress)
(C)Species: Arabidopsis thaliana (mouse-ear cress)
(C)Date: 0.02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
(C)Accession: H84698
(B)Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Neith, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
(Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
(A)Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
(A)Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-512 <STO>
;Cross-references: UNIPROT:082390; GB:AE002093; NID:93582333; PIDN:AAC35230.1; GSPDB:GN(
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                                                                                                 Query Match 42.6%; Score 43; DB 2; Best Local Similarity 47.4%; Pred. No. 59; Matches 9; Conservative 4; Mismatches 6
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A,Gene: gatA, RP152
C,Superfamily: indoleacetamide hydrolase
                                                                                                                                                                                                                                                                                   432 LFTIPASLAGLPCASVPAG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g29650
A;Map position: 2
C;Superfamily: hexuronate transporter
                                                                                                                                                                                                                                           1 LFTILLTLWTMRCSSTPSG 19
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

November 10, 2004, 11:27:01; Search time 20.7886 Seconds (without alignments) 525.871 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-17 101 1 LFTILITLWTWRCSSTPSG 19

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|   |        | Description  | Q8vgj6 mu | Q7tgs3 mus musculu |        | Q9rfy6 helicobacte |        | bordetel | 36     | æ      |        | Q9k438 streptomyce | Q7xmw5 oryza sativ | Q72g36 desulfovibr | 0        | Q6zlf8 oryza sativ | 0        |        |        | yersinia | 6 yersini | Q9km08 vibrio chol | Q8iwy0 homo sapien | Aaq88538 homo sapi | homo sa | Q8g7d8 bifidobacte | Q8z8j6 salmonella | Q8zr18 salmonella | P52484 caenorhabdi | _        | ce anopheles | bacillus | rhodopirel |
|---|--------|--------------|-----------|--------------------|--------|--------------------|--------|----------|--------|--------|--------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------|--------|----------|-----------|--------------------|--------------------|--------------------|---------|--------------------|-------------------|-------------------|--------------------|----------|--------------|----------|------------|
|   | ,      | QI           | Q8VGJ6    | Q7TQS3             | Q91Y12 | CDTA HELHP         | Q7W0R6 | Q7W2G6   | Q7WRD6 | Q82148 | OBECGe | Q9K438             | Q7XMW5             | Q72G36             | AAS94509 | Q6ZLF8             | BAC83009 | QBVJP0 | Q8ZCP2 | OSCID9   | AAS62946  | 09KM08             | OSIMYO             | AAQ88538           | Q9H8E9  | Q8G7D8             | 082806            | Q8ZR18            | UB21 CAEEL         | Q7PD60 . | Q7PDC6       | Q9LAF4   | Q7UI89     |
|   |        | DB.          | 8         | N                  | ~      | Н                  | ~      | N        | N      | N      | N      | ~                  | ~                  | 0                  | (7       | N                  | 7        | 7      | 7      | ~        | 7         | N                  | N                  | 0                  | ~       | <b>(1</b>          | 0                 | ~                 | Н                  | N        | N            | N        | (1)        |
|   | •      | Match Length | 315       | 318                | 946    | 231                | 391    | 408      | 410    | 252    | 373    | 522                | 558                | 719                | 719      | 80                 | 80       | 139    | 186    | 199      | 199       | 263                | 321                | 321                | 380     | 947                | 255               | 255               | 260                | 341      | 382          | 418      | 431        |
| æ | Query  | Match        | 53.5      | 53.5               | 48.0   | 47.5               | 47.5   | 47.5     | 47.5   | 46.5   | •      | •                  |                    |                    |          | 45.5               | •        | •      |        | •        | 45.5      | 45.5               | •                  | •                  |         | •                  | 45.0              | 45.0              | 44.6               | 44.6     | 44.6         | 44.6     | 44.6       |
|   |        | Score        | 54        | 54                 | 48.5   | 48                 | 48     | 48       | 48     | 47     | 47     | 47                 | 47                 | 47                 | 47       |                    |          |        | 46     | 46       | 46        | 46                 | 46                 |                    | 46      | 46                 |                   | 45.5              | 45                 | 45       | 4.5          | 4.5      | 45         |
|   | Result | No.          |           | 8                  | ٣      | 4                  | Ŋ      | 9        | 7      | œ      | თ      | 10                 | 11                 | 12                 | 13       | 14                 | 15       | 16     | 17     | 18       | 19        | 20                 | 21                 | 22                 | 23      | 24                 | 25                | 26                | 27                 | 28       | 29           | 30       | 31         |

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## ALIGNMENTS

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[1]
SEQUENCE FROM N.A.
STRAIN=ATCC 51449 / 3B1;
Protocadherin alpha 8.
Name=Pcdhal;
                                                                                                                                                                                                                                                               Cell 97:779-790(1999)
                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserv
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CDTA_HELHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanders K.; Submitted (UTN-2003) to the EMBL/GenBank/DDBJ databases. submitted (UTN-2003) to the EMBL/GenBank/DDBJ databases.

-1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-1 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

BMBL; ANS18686; ANF71986.1; .

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001884; F:receptor activity; IEA.

GO; GO:0001886; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; P:rhodopsin-like receptor protein signalin. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22974002; PubMed=14611657;
Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Trask B.J.;
"Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                  11arity 60.0%; Score 54; DB 2; Length 315; Conservative 3; Mismatches 3: Indel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 54; DB 2; Length 318; 60.0%; Pred. No. 4.7; 1ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRACTORY.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN RECEP_F1_2; 1.
G_PROTEIN RECEP_F1_2; 1.
G_PROTEIN RECEP_F1_2; 1.
SEQUENCE 315 A3, 35383 MW; A9C2A3E88501A179 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     071033.
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Olfactory receptor Olfr1418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        318 AA.
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091X12;
01-DEC-2001 (TEMBLE-1 19,
01-DEC-2001 (TEMBLE-1 19,
01-MAR-2004 (TEMBLE-1 26,
                                                                                                                                                                                                                                              3 TILLTLWIMRCSSTP 17
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Best Local Similarity
Matches 9; Conserv
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nes 9; Conserv
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SEQUENCE FROM N.A.
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Q7TQS3
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Putative membrane protein.
OrderedLocusNames=BPP0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 391 AA;
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SEQUENCE 408 AA
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01-0CT-2003
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07W2G6
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cytolethal distending toxin subunit
Ricin B-type lectin.
N-palmitoyl cysteine (Potential)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.5%; Score 48; DB 1; Length 231;
58.8%; Pred. No. 29;
iive 2; Mismatches 5; Indels
              Young V.B., Knox K.A., Schauer D.B., "Cytolethal distending toxin sequence and activity in the enterohepatic pathogen Helicobacter hepaticus."; Infect. Immun. 68:184-191(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
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Interpro; IPR008997; RicinB like.
Interpro; IPR000772; RicinB lectin.
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    WEDLINE=20072683; PubMed=10603386;
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231 CY
217 Ris
16 N-1
16 S-0
26021 MW;
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Matches 10; Conservative
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SIGNAL
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Q7WOR6;
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Catteno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevol M.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevol I.,

RA Achtwell T., Goble A., Hamlin N., Hauser H., Holtovy S., Jagels K.,

RA Fabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Rabbinowitsch E., Rutter S., Sanders M., Sunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

RA Umwin L., Whitchead S., Barrell B.G., Masskell D.J.;

RA Umwin L., Mitchead S., Barrell B.G., Masskell D.J.;

RA Umwin L., Mitchead S., Barrell B.G., Masskell D.J.;

RODGET STATE STATE Dinding; IEA.

Bordetella parapertussis and Bordetella bronchiseptica.";

RE EMBL; BX440423; ChE3975831;

RGO; GO:0005524; F:Protein Amino acid phosphorylation; IEA.

RINERPLOM, PRODGESS PROCOMES PROCOMES I.
Gaps
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 AA; 40841 MW; 31AAEAA8BF1F4B69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 LFAILLALATLGVAVYWWQRLTGTPSG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LFTILLTL-----WIMRCSSTPSG 19
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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21.526-331(2003).
EMBL; AP005034; BAC71021.1; -.
Interpro, IPR011046; WD40_like.
Complete proteome; Hypothetical protein.
SEQUENCE 252 AA, 26338 WW, 97AAF9911EB6F085 CRC64;
                                                                                                                                                                                                                                                                              STRAIN=MA-4680;
MEDILINE=22608306; PubMed=12692562;
NECA H. IShikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba
Sakaki Y., Hattori M., Omura S.;
                          Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitlis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.5%; Score 47; DB 2; Length 252; 57.1%; Pred. No. 46;
                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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EMBL; AE015755; AANS6176.1; -.
TIGR; SO3176; -.
     MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||| | : || |
235 VTLWTRRTAHTPGG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 57.1 tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., A Parkhill J., Sebaihia M., Preston A., Manroy S.D., Mungall K.L., Cerdeno-Tarraga A.-M., Temple L., James K.D., Haarris B., Quail M.A., A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharrell S., Satuares R., Squares S., Stevens K., Unwin L., Mitchead S., Barrell B.G., Maskell D.J.,

Comparative analysis of the genome sequences of Bordetella pertussis, New Park Comparative analysis of the genome sequences of Bordetella pertussis, New Park Comparative analysis of the genome sequences of Bordetella pertussis, New Park Comparative analysis of the genome sequences of Bordetella pertussis, New Park Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A. P. Comparative A.
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60
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
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082148;
001-JTM-2003 (TrEMBLrel. 24, Last sequence update)
01-JTM-2003 (TrEMBLrel. 24, Last sequence update)
01-JTM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedicousNames-SAV3310;
Streptiomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBL TaxID=33903;
Query Match 47.5%; Score 48; DB 2; Length 408; Best Local Similarity 44.4%; Pred. No. 50; Matches 12; Conservative 1; Mismatches 6; Indels
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44.4%; Pred. No. 50;
tive 1; Mismatches 6; Indels
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:000668; F:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
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SEQUENCE 410 AA; 42806 MW; 0BDC294518BD02A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative membrane protein.
OrderedLocusNames=BB0017;
                                                                                                                                                                                                                                                                                                           410 AA
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                                                                                                            1 LFTILLTL-----WIMRCSSTPSG 19
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Best Local Similarity
Matches 12; Conserv
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SEQUENCE FROM N.A.
STRAIN=MA-4680;
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Gaps

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Indels

o; Heidelberg J.F., Paulsen T.T., Nelson K.E., Gaidos B.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N.L., Methe B.A., Seshadri R., Ward N.L., Methe B.A., Scott J., Beanan M.J., Darkin B.T., Naugherry S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., Mhite O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., "Genome gequence of the dissimilatory metal ion-reducing bacterium Gaps Bacteria; Proteobacteria, Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella. NCBI\_TaxID=70863; ö DB 2; Length 373; Indels STRAIN=MR-1; MEDLINE=222297686; PubMed=12368813; DOI=10.1038/nbt749; 41298 MW; 51865EF2E6C4BB5A CRC64; 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Glycosyl transferase, group 1 family protein.
OrderedLocusNames=SO3176; 373 AA GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR001296; Glyco\_trans\_1.
Pfam; PF00534; Glycos transf\_1; I.
Complete proteome; Transferase. Query Match 46.5%; Score 47; DB Best Local Similarity 50.0%; Pred. No. 66; Matches 6; Conservative 5; Mismatches

RESULT 8

à d 92118 92100 9200 9200 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300 9300

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SEQUENCE
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In Nature 417:141-147(2002).

In Nature 417:141-147(2002).

R HSSP; P26514; 1KNM.

R GO; GO:0016787; F:hydrolase activity; IEA.

R InterPro; IPR002807; Richin Blectin.

R InterPro; IPR010997; Richin Blectin.

R InterPro; IPR010104; Stalidase.

R PRam; PF02012; BNR; 3.

R PRam; PF02012; BNR; 3.

R PRAM; FR00652; Richin Blectin; 3.

R PRAM; FR00652; Richin Blectin; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a; MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch E., Rajandrem M.A., Rutherford K.M., Rutter S., Rabbinowitsch E., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative bifunctional protein (Secreted sugar binding protein/sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902,
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                                                                                                                                                                                                                                                                                                                                                                                                                         hydrolase).
OrderedLocusNames=SCO1061; ORFNames=SCG22.07, SCG22.07c;
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PSS0231; RICIN B_LECTIN; 1.
proteome; Hydrolase.
SSS AA; 58835 MW; E78C9A88990B2786 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OSJNBA0040015.9 protein.
Name=OSJNBA0040015.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 AA.
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|LTALLSLWSQPASAAPVG 38
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nes 9; Conservative
                                            108 IWSVRCSNIPAG 119
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                                                                                                                                                                                                                             PRELIMINARY;
      8 LWTMRCSSTPSG 19
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Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Liu X., Lu Y., Mu J., Lu Y., Zhang L.S., Yu S., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen L., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lu G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Rang H., Chen X., Shao C., Sun Y., Hu Q., Zhang Y., Lan L., Ling C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio.
NCBL_TaxID=882,
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Pred. No. 96;
7; Mismatches 4; Indels
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558 AA; 61560 MW; CB9ADAE249570AC8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box histidine kinase.
OrderedLocusNames=DVU0025;
                                                                                                                                                                                                    "Sequence and analysis of rice chromosome 4."; Nature 420:316:320(2002).
EMBL; ALG06655; CAE04419.2; -. Gramene; Q7XMW5; -.
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Best Local Similarity 35.3%;
Matches 6, Conservative
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Gaps

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Length 80;

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Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003753, BAC83009.1; -.
Hypothetical protein.
SEQUENCE 80 AA; 8162 MW; B0727F9BF8014D9B CRC64;
                                                                                                                                                                                                                                                                                            45.5%; Score 46; DB 2; 50.0%; Pred. No. 22; trive 3; Mismatches
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Best Local Similarity 50.0°
Matches 8; Conservative
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SEQUENCE FROM N.A.
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02-MAR-2004
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PubMed=15077118;
Rolonay J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Rolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinked L.M.,
Daughberty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.,
Mat. genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.",
BMBL, AE017309; AAS945091; -.
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OS-UTL-2004 (TERMELrel. 27, Last sequence update)
OS-UTL-2004 (TERMELrel. 27, Last sequence update)
OS-UTL-2004 (TERMELrel. 27, Last annotation update)
Hypothetical protein OJ1339_B08.6.

Name=OJ1339_B08.6.

Name=OJ1339_B08.6.
Name=OJ139_B08.6.
Strestophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryzea.
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Desulfovibrionaceae; Desulfovibrio.
NCBI_TaxID=882;
SMART; SM00091; PAS; 3.
TIGREAM'S, TIGROSUS9; Sensory_box; 3.
PROSITE; PSS0109; HIS, KIN; 1.
PROSITE; PSS0113; PAC; 2.
Complete proteome; Kinase; Phosphorylation; Sensory transduction; Iransferase.
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26-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Sensory box histidine kinase.
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LCVVLLTLWRLRASS 68
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Best Local Similarity 60.0°
Matches 9; Conservative
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                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza, Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.5%; Score 46; DB 2; Length 80; 50.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003753; BAC83009.1; --
Hypothetical protein.
SEQUENCE 80 AA; 8162 MW; B0727F9BF8014D9B CRC64;
                                           02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OJ1339_B08.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 10, 2004, 12:27:18 Job time : 23.7886 secs
     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0°
Matches 8, Conservative
PRELIMINARY;
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Sequence 867, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENUENCE 1596-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1999-04-01
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US-09-538-092-867
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                                                                                                                        November 10, 2004, 11:41:17; Search time 8.33951 Seconds (without alignments) 222.664 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-538-092-867
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-880B-1
US-09-622-823-1
US-09-032-523-7
US-09-032-523-7
US-09-032-633-7
US-09-157-349-9
US-08-487-942-6
US-08-487-942-6
US-08-487-942-6
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US-08-487-942-7
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US-09-377-497-70
US-09-422-869-28
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Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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136
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Match Length DB
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Patent No. 52
Sequence 2, 3
Sequence 3, 7
                                       Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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GENERAL INFORMATION:
APPLICANT: HORIKGAMA, YUKIO
APPLICANT: HORIKGAMA, YUKIO
APPLICANT: COZA, NAOHISA
APPLICANT: COZA, NAOHISA
APPLICANT: COZA, NAOHISA
APPLICANT: SERSTAN, SEAMUS
APPLICANT: SERSTAN, SEAMUS
APPLICANT: RENICHI
APPLICANT: ARICHI
APPLICANT: MINIS, CRAIG
INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
TITLE APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
BARLIER APPLICATION NUMBER: 60/134,175
BARLIER APPLICATION NUMBER: 60/134,175
BARLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENT VET. 2.0
SEQ ID NO 2: 2.0
SEQ ID NO 2: 2.1
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          US-09-653-839-8

US-10-202-619-8

US-10-202-619-8

US-09-653-839-6

US-09-653-839-4

US-09-653-839-4

US-09-653-839-2

US-09-653-839-2

US-09-653-839-2

US-09-157-349-1

US-09-157-349-1

US-09-157-349-1

US-09-157-349-1

US-09-248-796A-24140

S2-8828-1

US-08-978-285-3

US-08-978-285-3
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Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 28; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09422869 Patent No. 6235481
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-422-869-22
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16; Conservative
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; ORGANISM: mouse
US-09-308-345A-48
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US-09-422-869-24
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LENGTH: 821
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Patent No. 656665
GENERAL INFORMATION:
APPLICANT: BOBHN, Thomas;
APPLICANT: BOBHN, Thomas;
TITLE OF INVENTION: No. 656965el calpains, their preparation and use
FILE REFERENCE: 0050/47576
CURRENT APPLICATION WUMBER: US/09/308,345A
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: WordPerfect v. 6.1
SEQ ID NO 47
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                                                                                                                                                                                                                                                            100.0%; Score 136; DB 4; Length 714; 100.0%; Pred. No. 3.8e-12; tive 0; Mismatches 0; Indels (
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Patent No. 658292
GENERAL INFORMATION:
APPLICANT: FUXIAGE, Chiho
APPLICANT: FUXIAGE, Chiho
TITLE OF INVENTION: NOVEL CALPIN AND DNA ENCODING THE SAME
TILE REFERENCE: 2000-1125A/WMC/00177
CURRENT APPLICATION NUMBER: US/09/622,880B
CURRENT FILING DATE: 1908-08-24
PRIOR APPLICATION NUMBER: UP 10-049430
PRIOR APPLICATION NUMBER: 19 10-049430
NUMBER OF SEQ ID NOS: 16
SEQ ID NO : LENGTH: 757
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Best Local Similarity 96.4%; Pred. No. 6.1e-11;
Matches 27; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                555 AGEDMEISVKELRTILNRIISKRKDLRT 582
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PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SEQ ID NO 867
LENGTH: 714
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57.1%;
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; ORGANISM: Sprague-Dawley rat
US-09-622-880B-1
                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-308-345A-47
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APPLICANT: FUKIAGE, Chiho
APPLICANT: AZUMA, MIEGENYOShi
TITLE CALTENAT: AZUMA, MIEGENYOShi
FILE REFERENCE: 2000-1125A/WMC/00177
CURRENT APPLICATION NUMBER: US/09/622,880B
CURRENT APPLICATION NUMBER: US 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 15
LENGTH: 821
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 821;
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Pred. No. 6.8e-06;
7; Mismatches 5; Indels
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69.9%; Score 95; DB 4; Le
Best Local Similarity 57.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 7; Mismatches 5;
                                                 598 AGDDMEICADELKOVUNTVVNKHKDLKT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 AGDDMEICADELKNVLNTVVNKHKDLKT 689
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US-09-622-880B-15
Sequence 15, Application US/09622880B
Patent No. 6582932
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Patent No. 6235481
GENERAL INFORMATION
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                  69.98;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: p94 protein US-09-622-880B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: No. 6582932way rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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STREET:
CITY: Pa
STATE: C
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| Sequence 972, Application US/09538092
| Patent No. 675314
| GENERAL INCORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Giot, Loic
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
| TITLE OF INVENTION: DETE: 15966-542
| CURRENT APPLICATION NUMBER: 06/127,352
| PRIOR PILLING DATE: 2000-03-29
| PRIOR PILLING DATE: 1999-04-01
| PRIOR PILLING DATE: 2000-02-01
| PRIOR PILLING DATE: 2000-02-01
| PRIOR PILLING DATE: 2000-02-01
| PRIOR PILLING DATE: 2000-02-01
| SERIOR PILLING DATE: 2000-02-01
| PRIOR SEQ ID NOS: 1387
| SOFTWARE: CuraPatSeqFormatter Version 0.9
| SEQ ID NO 972
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            APPLICANT: COX, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: CTANI, NENICHI
APPLICANT: OTANI, RASICHI
APPLICANT: HALL, GRAEME I.
APPLICANT: HELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
TITE REFERENCE: ARCD: 307
CURRENT FALLIGE DATE: 1999-10-21
CURRENT FALLIGE DATE: 1999-10-21
SARLIER PELICATION NUMBER: 60/134,175
SARLIER PILICAN NUMBER: 60/134,175
SARLIER PILICE DATE: 1999-05-13
NUMBER OF SEQ. ID NOS 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.1%; Score 94; DB 4; Length 821; Best Local Similarity 57.1%; Pred. No. 9.7e-06; Matches 16; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.1%; Score 94; DB 3; Length 821; ilarity 57.1%; Pred. No. 9.7e-06; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P20807US-09-538-092-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 AGDDMEICADELKKVLNTVVNKHKDLKT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 AGDDMEICADELKKVLNTVVNKHKDLKT 689
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Sequence 1, Application US/09032523
Parent No. 6232454
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
NAOHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-538-092-972
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APPLICANT: COCIETY Neal: C.
APPLICANT: COCIETY Neal: C.
APPLICANT: COCIETY Neal: C.
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
WINNERS OF SEQUENCES: 9
COCREGORDENCE AND PROJECTIONS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF COCKETS OF
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107 AGDDMEVSATELMNILNKVVTRHPDLKT 134
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                  REFERENCE/DOCKET NUMBER: PF-0479 US
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TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09802633
Patent No. 6627605
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
                                                                                                                                                            LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID.NO:
SEQUENCE CHARACTERISTICS:
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IMMEDIATE SOURCE:
LIBRARY: GenBank
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; LIBRARY: GenBank
; CLONE: 164403
US-09-032-523-7
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US-09-802-633-7
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESEO for Windows Version 2.0
CURENT APPLICATION NURBER: US/09/802,633
FILING DATE: 08-Mar-2001
.CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/032,523
FILING DATE: Unknown:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Fatent No. 6222454
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOILGY, Neil C.
APPLICANT: Baugh, Mariah
ITILE OF INVENTION: HUYAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 1 COYCE Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 AGPDMEVGATDLMNILNKVLSKHKDLKT 116
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CLONE: 456855
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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Matches 16; Conserva
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CLASSIFICATION:
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Length 266;
Query Match 66.9%; Score 91; DB 3; Length 266
Best Local Similarity 53.6%; Pred. No. 7.2e-06;
Matches 15; Conservative 8; Mismatches 5; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/802,633
FILING DATE: 08-Mar-2001
CLASSIFICATION: -Unknown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,523
FILING DATE: -Unknown-
ATTORNEY/ABORT INFORMATION:
ARGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guegler, Karl
Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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STREET: 3174 Porter Drive
CITY: Palo Alto
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| Sequence 9, Application US/08835099A
| Patent No. 5874277
| GENERAL INFORMATION:
| APPLICANT: SHINTANI, Yasushi
| APPLICANT: NISHI, Kaznorii
| APPLICANT: NISHI, Kaznorii
| TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
| TITLE OF INVENTION: AND USE
| NUMBER OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
| STREET: 130 Water Street
| COUNTRY: USA
| COUNTRY: USA
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.9%; Score 91; DB 2; Length 268; Best Local Similarity 53.6%; Pred. No. 7.2e-06; Matches 15; Conservative 8; Mismatches 5; Indels
                                                                                    Length 266;
                                                                                    Query Match 66.9%; Score 91; DB 4; Length 266 Best Local Similarity 53.6%; Pred. No. 7.2e-06; Matches 15; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZUDIATION OF THE PORM:
MEDIUM TYPE: Diskette
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099A
FILING DATE: US-4APR-1997
CLASSIFICATION DATE: 083649/1996
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTOMNEY/AGENT INFORMATION:
NAME: RESHICK DAVIG S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-523-3400
TELEPAX: 617-523-3400
TELEPAX: 617-523-6440
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                                                                                                                                                                                1 AGEDMEISVKELRTILNRIISKHKDLRT 28
; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-802-633-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-157-349-9
; Sequence 9, Application US/09157349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 268 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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PREDICATIVE NISTRY, Vasuable APPLICANT NISTRY, Vasuable APPLICANT NAMEWORD, COMBINED THIRD OF INTENTION NOVEL PROTEINS, THEIR PRODUCTION THIRD OF INTENTION NOVEL PROTEINS, THEIR PRODUCTION THIRD OF INTENTION NOVEL PROTEINS, THEIR PRODUCTION THIRD OF INTENTION NOVEL PROTEINS, THEIR PRODUCTION THIRD OF INTENTION NOVEL PROTEINS & CUSNAM, ILP STREET, 130 Marc Street COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMPUTER. HA COMP
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Query Match 59.6%; Score 81; DB 1; Length 251; Best Local Similarity 53.6%; Pred. No. 0.00022; Matches 15; Conservative 8; Mismatches 5; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,525
FILING DATE: 07-OCT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/487,942
FILING DATE: 07-UN-1995
ATTORNEY/AEBNT INFORMATION:
NAME: BEOWN, SCOLE A.
REGISTRATION NUMBER: 32,724
REFERENCY DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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TELEPHONE: (617)
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1 AGEDMEISVKELRTILNRIISKHKDLRT 28

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Gaps 0;

Search completed: November 10, 2004, 12:32:30 Job time : 8.33951 secs

Sequence 122, App Sequence 257, App Sequence 258, App

Sequence 24, Appli Sequence 5, Appli Sequence 124, Appli Sequence 101, Appli Sequence 101, Appli Sequence 101, Appli Sequence 221, Appli Sequence 221, Appli Sequence 8, Appli Sequence 6, Appli Sequence 19, Appli Sequence 19, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 28, Appli Sequence 12, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli

Scoring table:

Sequence:

Run on:

Total number

Searched:

Database

Sequence 13, App.

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Sequence 18, Application US/10092750;
Publication No. US20030032157A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.;
APPLICANT: Alphi, Julia
APPLICANT: Might, Martin C.;
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1;
FILE REFERENCE: 50036/050002;
CURRENT APPLICATION NUMBER: US/10/092,750;
CURRENT APPLICATION NUMBER: US/10/092,750;
PRIOR APPLICATION NUMBER: US/10/092,750;
PRIOR FILING DATE: 2001-03-08;
NUMBER OF SEQ ID NOS: 253;
SOFTWARE: FastSEQ for Windows Version 4.0;
INNOTH: 28
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S US-10-336-472-122

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US-10-080-334-254

US-10-080-334-254

US-10-116-517-24

US-10-116-517-24

US-10-136-685-5

US-10-390-685-5

US-10-390-685-5

US-10-36-685-5

US-10-36-685-5

US-10-621-263-1

US-09-925-301-101

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100.0%; Pred. No. 1.5e-12;
iive 0; Mismatches 0;
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Patent No. US20020150896A1
GENERAL INFORMATION:
       28; Conservative
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US=09-768-877-22
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Matches
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Sequence 6, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 260, Appli
Sequence 260, Appli
Sequence 259, Appli
Sequence 11, Appli
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                                                                                                                                                          November 10, 2004, 15:53:52; Search time 27.0062 Seconds (without alignments) 366.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/Der_Maw PuB.pep:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-116-515-6

6 US-10-408-753-1337

6 US-10-116-519-8

5 US-10-116-519-9

6 US-10-116-519-9

7 US-10-10-117

5 US-10-080-334-259

5 US-10-080-334-259

6 US-10-333-574-1
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US-09-768-877-22
                                                                                                                                                                                                                                                                                  136
1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                                                                                                                                                                                                                                                                                                                                                                                      1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Gaps

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Indels

Length 28;

Score

Result

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US-10-116-519-8
Sequence 8, Application US/10116519
Sequence 8, Application US/10116519
Sequence 8, Application No. US2030114373A1
Sublication No. US2030114373A1
GENERAL INCRMATION:
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
FILE REFERENCE: D0124 NP
CURRENT APPLICATION NUMBER: US/10/116,519
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/281,253
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
                                                                                                     APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: FOOTNUTCHEENTION ENCORTING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
TITLE OF INVENTION: SUPERFAMILY, Protease-42
FILE REFERENCE: D0219np
CURRENT APPLICATION WINBER: US/10/390,585
CURRENT RAPLICATION NUMBER: US. 60/364,941
PRIOR APPLICATION NUMBER: U.S. 60/364,941
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEG ID NOS: 102
SOFTWARE: PatentIn version 3.2
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APPLICANT: Zhang, Bing
APPLICANT: Glason, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TENETS DIVING MATERIAL PROTECME
FILE REFERENCE: 660088.465
TITLE OF INVENTION: UNDER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077-64-04
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 1337
LENGTH: 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 136; DB 15; Best Local Similarity 100.0%; Pred. No. 7.1e-11; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S55 AGEDMEISVKELRTILNRIISKHKDLRT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 AGEDMEISVKELRTILNRIISKHKDLRT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGEDMEISVKELRTILNRIISKHKDLRT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1337, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-10-390-585-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-408-765A-1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: HOMO
US-10-408-765A-1337
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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Publication No. US20030114373A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: D0124 NP

FILE REFERENCE: D0124 NP

CURRENT APPLICATION NUMBER: US/10/116,519

CURRENT FILING DATE: 2002-04-03

PRIOR PLILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/281,253

PRIOR PLILING DATE: 2001-05-04

PRIOR PLILING DATE: 2001-05-04

PRIOR PLILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

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PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
"ALISA"

"NANCY J.

SREENAN, SEAMUS

"FLICANT: TANN. SEAMUS

"FLICANT: OTANI, KENTCHI

APPLICANT: BELL, GRAENE I.

APPLICANT: BELL, GRAENE I.

TITLE OF INVENTION: WEHFODS OF TREATMENT OF TYPE 2 DIABETES

FILE REFERENCE: ARCI307

CURRENT APPLICATION NUMBER: US/09/768,877

CURRENT FILING DATE: 1999-10-21

PRIOR PILING DATE: 1999-10-21

PRIOR PILING DATE: 1999-10-21

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 22

IENGTH: 714

TYPE: PTT

ORGANISM: ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 136; DB 9; Length 714;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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100.0%; Score 136; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 AGEDMEISVKELRTILNRIISKHKDLRT 582
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CAGANISM: Homo sapiens
US-10-116-519-6
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; Sequence 3, Application US/10390585; Publication No. US20040014093A1; GENERAL INFORMATION:

US-10-390-585-3 RESULT 4

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APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Schenberg, Mark
APPLICANT: Stone, David June
APPLICANT: Stone, David June
APPLICANT: Stone, David June
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: URING THE SAME
FILE OF INVENTION: USING THE SAME
FILE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT APPLICATION NUMBER: US/209-25
PRIOR PILING DATE: 2001-02-14
PRIOR PAPLICATION NUMBER: 60/265,587
PRIOR PLING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/272,409
PRIOR PLING DATE: 2001-03-28
PRIOR PLING DATE: 2001-01-08
PRIOR PLING DATE: 2001-01-08
PRIOR PLING DATE: 2001-01-08
PRIOR PLING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,409
PRIOR PLING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/272,477
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
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                                                                                                                                                                                           Length 709;
                                                                                                                                                                                     Query Match
69.9%; Score 95; DB 14; Length 70
Best Local Similarity 57.1%; Pred. No. 5.9e-05;
Matches 16; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                           1 AGEDMEISVKELRTILNRIISKHKDLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vernet, Corine AM
Li, Li
Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaolia Sasha
Edinger, Shlomit R
MacDougall, John R
Matyankar, Uriel M
Parturajan, Meera
Shimkets, Richard A
Perturajan, Velizar T
Zerhusen, Bryan D
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baumgartner, Jason
Herrman, John L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lepley, Denise M
Smithson, Glennda
                                                                           TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-519-9
; SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
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Publication No. US20030114373A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN

TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF

TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF

TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF

TITLE OF INVENTION NUMBER: US 60/281, 253

PRIOR PELICATION NUMBER: US 60/281, 253

PRIOR PELICATION NUMBER: US 60/286, 180

PRIOR PELICATION NUMBER: US 60/296, 180

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620

PRIOR PELICATION NUMBER: US 60/300, 620
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Sequence 11, Application US/10390585
Publican No. UG20040014093A1
GENERAL INFORMATION:
APPLICANT: BISISCL—Myers SQUIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN TITLE OF INVENTION NUMBER: US/10/390,585
CURRENT APPLICATION NUMBER: US/0/304,941
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 102
SOPTWARE: PARCENT NOVEL OF SEQ ID NOS: 102
SOPTWARE: PARCENT NOVEL OF SEQ ID NOS: 102
SOPTWARE: PARCENT NOVEL OF SEQ ID NOS: 102
SOPTWARE: PARCENT NOVEL OF SEQ ID NOS: 102
SOPTWARE: PARCENT NOVEL OF SEQ ID NOS: 102
SEQ ID NO 11
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94.9%; Score 129; DB 14; Length 713;
Best Local Similarity 92.9%; Pred. No. 7.3e-10;
Matches 26; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 94.9%; Score 129; DB 15; Length 713; 1 Similarity 92.9%; Pred. No. 7.3e-10; 26; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                     ; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/296,180
; PRIOR FILING DATE: 2001-06-06
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 8
; LENGTH: 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                TYPE: PRT

ORGANISM: Mus musculus
US-10-116-519-8
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Best Local S
Matches 26
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US-10-080-334-260
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APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Schusen, Bryan D
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-275
CURRENT APPLICATION NUMBER: US/10/080,334
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR APPLICATION NUMBER: 60/312,712
PRIOR APPLICATION NUMBER: 60/311,980
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/330,307
PRIOR APPLICATION NUMBER: 60/278,76
PRIOR APPLICATION NUMBER: 60/278,76
PRIOR APPLICATION NUMBER: 60/278,76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGEDMEISVKELRTILNRIISKHKDLRT 28
PRIOR APPLICATION NUMBER: 60/291,6/2
PRIOR FILING DATE: 2001-05-17
PRIOR PLING DATE: 2001-018
PRIOR PLING DATE: 2001-10-18
PRIOR PELICATION NUMBER: 60/265,530
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 117
LENGTH: 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 260, Application US/10080334
Publication No. US20040002584A1
GENERAL INFORMATION:
APPLICANT: Pena, Carol E. A.
APPLICANT: Shimkets, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR FILING DATE: 2001-08-10
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FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/276,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gangolli, Esha A
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu, Xiachong
Baumgartner, Jason C.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casman, Stacie J
Boldog, Ferenc L
Furtak, Katarzyna
Tchernev, Velizar T
Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shenoy, Suresh G
Kekuda, Ramesh
Spyrek, Kimberly A
Vernet, Cornine A. M.
Walyankar, Uriel M
Guo, Xiaojia
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                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Rattus norvegicus US-10-051-874-117
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US-10-080-334-260
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. US20030232349A1 5155802CD1 US-10-274-639-1
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GENERAL INFORMATION:
APPLICANT: INCYEE GENOMICS, INC.
APPLICANT: DELEGEANE, April J. A.; Lu, Dyung Aina M.
APPLICANT: AFFALIA, April J. A.; Lu, Dyung Aina M.
APPLICANT: AFFALIA, April J. A.; Lu, Dyung Aina M.
APPLICANT: ANGTEN, Danniel B.; LEE, Ernestine A.
APPLICANT: ANGTEN, Danniel B.; LEE, Ernestine A.
APPLICANT: MGTYEN, Danniel B.; LEE, Ernestine A.
APPLICANT: MGTYEN, Danniel B.; LEE, Ernestine A.
APPLICANT: MGTYEN, Danniel B.; LEE, Ernestine A.
APPLICANT: MGTYEN, Mariah A.; YUE, Henry
APPLICANT: MGTYEN, Mariah R.; BOROMSKY, Mark L.
APPLICANT: POLICKY, Jennieler L.; RANKUMAR, Jayalaxmi, APPLICANT: DING, LI; KEARNEY, Liam
APPLICANT: MGTHAN, MARIAH, Mariah R.; BOROMSKY, Mark L.
APPLICANT: SANGANANALA, Madhusudan M.; YAO, Monique G.
APPLICANT: SANGANANALA, Mathusudan M.; YAO, Monique G.
APPLICANT: SANGANANALA, Mathusudan M.; YAO, Monique G.
APPLICANT: SANGANANALA, Mathusudan M.; YAO, Monique G.
APPLICANT: AZIMZAI, Yalda; LU, Yan
TILLE DY INVERTY DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/220,063
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR PLICATION NUMBER: US 60/221,568
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
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PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-17
PRIOR PRICATION NUMBER: US 60/227,568
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR PRICATION NUMBER: US 60/227,568
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PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,544
PRIOR PELING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
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PRIOR PELING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 42
SOFTHARE: PERL PROGRAM
LENGTHARE: PROBLAM
TYPE: PRT
TYPE: PRT
CREANIES:
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GENERAL INFORMATION:
APPLICANT: DELEGEANE, Angelo M.; GANDHI, Ameena R.;
APPLICANT: HAFALIA, April J. A.; LU, Dyung Aina M.;
APPLICANT: PATTERSON, Chandra; TRIBOULEY, Catherine M. APPLICANT: DAS, Deboptiya; RALLICK, Deborah A.;
APPLICANT: MGUYEN, Danniel B.; LEE, Ernestine A.;
APPLICANT: MGUYEN, Danniel B.; LEE, Ernestine A.;
APPLICANT: MGUYEN, Danniel B.; LEE, Ernestine A.;
APPLICANT: MGUYEN, Janiek K.; GRIFFIN, Jennifer A.;
APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi, APPLICANT: PANG, Junming; THANGAVELU, Kavitha APPLICANT: DING, Li; KRANEY, Lian APPLICANT: DAUGHN, Mariah R.; BOROWSKY, Mark L.; APPLICANT: DAUGHN, Mariah R.; BOROWSKY, Mark L.; APPLICANT: DAUGHN, Mariah R.; BOROWSKY, Mark L.; APPLICANT: LAL, Preeti G.; LEE, Sally, APPLICANT: HODD, Stephen; LO, Terence P.; APPLICANT: AZINZAI, Yalda; LU, Yan
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PL-O167 USA
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGEDMEISVKELRTILNRIISKHKDLRT 28
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PRIOR APPLICATION NUMBER: PCT/US01/22397
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/221,680
PRIOR APPLICATION NUMBER: 60/278,796
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/281,521
PRIOR APPLICATION NUMBER: 60/276,677
PRIOR APPLICATION NUMBER: 60/276,677
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-080-334-259
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Gaps

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Query Match 69.1%; Score 94; DB 15; Length 773; Best Local Similarity 57.1%; Pred. No. 9.2e-05; Matches 16; Conservative 7; Mismatches 5; Indels
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PRIOR APPLICATION NUMBER: 60/291,765
PRIOR FILING DATE: 2001-05-17
PRIOR PRING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/276,400
PRIOR APPLICATION NUMBER: 60/276,400
PRIOR PRING DATE: 2001-03-16
PRIOR PRING DATE: 2001-03-16
PRIOR PRING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 388
SEQ ID NO 86
ILENGTH: 773
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-080-334-86
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APPLICANT: Banquagather. Jason C.
APPLICANT: Banquagather. Jason C.
APPLICANT: Gerlach, Valerie
APPLICANT: Spaderna, Steven K
APPLICANT: Serbusen, Bryan D
TITLE OF INVENTION: Proceeins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
CURRENT APPLICATION NUMBER: US/10/080, 334
CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                                                                                   Query Match 69.1%; Score 94; DB 15; Length 767; Best Local Similarity 57.1%; Pred. No. 9.1e-05; Matches 16; Conservative 7; Mismatches 5; Indels
                                                                                   ; FEATURE:
; NAME/KEY: misc feature
; OTHER OTHER US: 5155802CD1
US-10-333-574-1
                                                                                                                                                                                                                                                                                                                                                            1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-02-1
RIOR APPLICATION NUMBER: 60/270,523
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR APPLICATION NUMBER: 60/322,712
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-17
PRIOR PLICATION NUMBER: 60/311,980
PRIOR PLING DATE: 2001-09-18
PRIOR PELING DATE: 2001-01-8
PRIOR PLING DATE: 2001-01-8
PRIOR PLING DATE: 2001-01-8
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-04-8
PRIOR PLING DATE: 2001-04-8
PRIOR PLING DATE: 2001-04-8
PRIOR APPLICATION NUMBER: 60/281,521
PRIOR PLING DATE: 2001-04-8
PRIOR FLING DATE: 2001-04-8
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PRIOR FILING DATE: 2001-08-10
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RIOR APPLICATION NUMBER: 60/270,220
PRIOR FILING DATE: 2001-02-21
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CATION NUMBER: 60/318,526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/10080334
Publication No. US20040002584A1
GENERAL INFORMATION:
APPLICANT: Pena, Carol E. A.
APPLICANT: Shimkets, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gangolli, Esha A
Padigaru, Muralidhara
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Boldog, Ferenc L
Furtak, Katearzyna
Tchernev, Velizar T
Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shenoy, Suresh G
Kekuda, Ramesh
Spyrek, Kimberly A
Vernet, Cornine A. M.
Malyankar, Uriel M
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Susev, Vladimir Y
                           TYPE: PRT
ORGANISM: Homo sapiens
        LENGTH: 767
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APPLICANT: Zerhusen, Bryan D. APPLICANT: Zhong, Mei TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-2533C CURRENT APPLICATION NUMBER: US/10/336,472
Sequence 122, Application US/10336472
Publication No. US20040043929A1
GENERAL INFORMATION:
                                                                                                                                                     APPLICANT: Anderson, David W. APPLICANT: Anderson, David W. APPLICANT: Ballinger Robert A. APPLICANT: Ballinger, Tobert A. APPLICANT: Barngartner, Jason C. APPLICANT: Casman, Stacie J. APPLICANT: Chant, John S. APPLICANT: Gangolli, Esha A. APPLICANT: Edinger, Shomit R. APPLICANT: Ellerman, Karen APPLICANT: Ellerman, Karen APPLICANT: Gunther, Valerie APPLICANT: Gunther, Dennifer A. APPLICANT: Gunther, Brik APPLICANT: Gunther, Brik APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: G
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Ichernev, Velizar T.
Vernet, Corine A.M.
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Millet, Isabelle
Padigaru, Muralidhara
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Spaderna, Steven K.
Shinkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Stone, David J.
Shenoy, Suresh G.
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MacDougall, John R.
Mishra, Vishnu
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CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-18
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PRIOR PLING DATE: 2001-12-18
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PRIOR PLING DATE: 2002-02-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%; Pred. No. 9.2e-05; Matches 16; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-336-472-122
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614 AGDDMEICADELKKVLNTVVNKHKDLKT 641 1 AGEDMEISVKELRTILNRIISKHKDLRT 28 g

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0; Gaps

Search completed: November 10, 2004, 16:36:02 Job time: 28.0062 secs

lodes Janua agod sint

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

November 10, 2004, 11:36:51; Search time 5.66049 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-18 136 1 AGEDMEISVKELRTILNRIISKHXDLRT 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                | calpain (EC 3.4. | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | EQ<br>CE | GGDEF family prote | plasma protein S p | endopeptidase Clp | type I restriction | hypothetical prote | lactosid | plasma protein S p | mycin synt |      | red hypot | ui. | plasma protein S p |
|----------------------------|------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|----------|--------------------|------------|------|-----------|-----|--------------------|
|                            | <u>: E</u>       | A24815    | 857195    | СІСНН     | 857196    | B34488    | CIHUH3    | A55143    | A34466    | CIPGL     | CIRBL     | CIHOL     | CIHUH2    | S38361    | B24815    | S57194    | A48764   | D82396             | KXMSS              | E72345            | 873820             | m                  | T05687   | KXBOS              | 459        | SO.  | N         | 젊   | ⊢                  |
| DB                         | !                |           |           |           |           | <b>1</b>  |           |           |           |           |           |           |           |           |           |           |          |                    |                    |                   |                    |                    |          |                    |            | (7   |           |     |                    |
| %<br>Query<br>Match Length | 714              | 320       | 586       | 705       | 810       | 821       | 821       | 184       | 263       | 266       | 266       | 268       | 700       | 700       | 422       | 700       | 703      | 339                | 675                | 203               | 543                | 4077               | 1036     | 675                | 9376       | 346  | 416       | 646 | 675                |
| *<br>Query<br>Match        |                  | φ.        | è.        | 4.        | 4         | 6.69      | σ.        | è.        | 9         | 9         | 9         | ė.        | 6         | e.        | œ.        | ω.        | ö        | ä                  |                    |                   | 40.4               |                    | 6        | 8                  | φ.         | 37.5 | ۲.        | 7   | 7.                 |
| Scor                       | l m              | 0         | 117       | 4         | 97        | 95        | 94        | 91        | 16        | 91        | 16        | 91        | 81        | 81        | 80        | 80        | 68       | 57                 | 56                 | 55.5              | 55                 | 55                 | 53       | 52                 | 52         | 51   | 51        | 51  | 51                 |
| Result<br>No.              |                  | 8         | ٣         | 4         | Ŋ         | 9         | 7         | 80        | 6         | 10        | 11        | 12        | 13        | 14        | 15        | 16        | 17       | 18                 | 19                 | 20                | 21                 | 22                 | 23       | 24                 | 25         | 56   | 27        | 28  | 29                 |

| plasma protein S p | endopeptidase cip<br>endopeptidase cin | hypothetical prote | electron transfer | MAPK-activated pro | hypothetical prote | mitogen-activated | plasma protein S p | antiviral protein | pipecolate-incorpo | mycosubtilin synth | translation elonga | syntaxin 11 - huma | adenylosuccinate l | probable adenylosu |
|--------------------|----------------------------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| KXHUS              | F81098                                 | S05299             | D69620            | T34519             | B70215             | JC5952            | S53434             | S58819            | T30227             | T44807             | B70389             | JE0094             | C75033             | H71135             |
| <b>H</b> (         | N C                                    | v (4               | α                 | N                  | 0                  | N                 | N                  | ~                 | 7                  | α                  | N                  | ~                  | ~                  | 73                 |
| 676                | 176                                    | 275                | 325               | 339                | 411                | 473               | 642                | 1432              | 1541               | 5369               | 582                | 287                | 450                | 450                |
| 37.5               | 37.1                                   | 36.8               | 36.8              | 36.8               | 36.8               | 36.8              | 36.8               | 36.8              | 36.8               | 36.8               | 36.4               | 36.0               | 36.0               | 36.0               |
| 51                 | 00 c                                   | 50<br>50           | 20                | S<br>0             | 50                 | 20                | 20                 | 20                | 20                 | 20                 | 49.5               | 4,0                | 49                 | 49                 |
| 80                 | 31                                     | 33.8               | 34                | 35                 | 36                 | 37                | 38                 | 39                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

| CIHUM  Calpain (BC 3.4.22.17) large chain 1 [validated] - human  Calpain (BC 3.4.22.17) large chain 1 [validated] - human  NyAlternate names: calpain chain L-1; calpain I catalytic chain; low-calcium requiring, C  NyAlternate names: calpain chain L-1; calpain I catalytic chain; low-calcium requiring, C  NyAlternate names: calpain spains (man)  C;Species: Homo appiens (man)  C;Accession: A26213, A36740; S10591  R;Aoki, K.; Imajoh, S.; Ohno, S.; Emori, Y.; Koike, M.; Kosaki, G.; Suzuki, K.  FEBS Lett. 205, 313-317, 1986  A;Title: Complete amino acid sequence of the large subunit of the low-Ca2+-requiring forn  A;Reference number: A26213; MUID:86301172; FMID:3017764 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| A; Molecule type: mRNA<br>A; Residues: 1-714 < AOK><br>A; Cross-references: UNIPROT: P07384; EMBL: X04366; NID: 929663; PIDN: CAA27881.1; PID: 929664<br>A; Cross-references: UNIPROT: P07384; EMBL: X04106; NID: 929663; PIDN: CAA27881.1; PID: 929664<br>B; Kunimatsu, M.; Higashiyama, S.; Sato, K.; Ohkubo, I.; Sasaki, M.<br>Biochem. Biophys. Res. Commun. 164, 875-882, 1989<br>A; Title: Calcium dependent cysteine proteinase is a precursor of a chemotactic factor for<br>A; Reference number: A36740; WUID: 90056492; PMID: 2554904                                                                                                                                                 |
| A; Molecule type: protein<br>A; Residues: 2-10 «KUN»<br>A; Experimental source: erythrocytes<br>R; Sorimachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Minami, Y.; St.<br>Biol. Chem. Hoppe-Seyler 371 (Suppl.), 171-176, 1990<br>A; Ittle: A novel member of the calcium-dependent cysteine protease family.<br>A; Reference number: S10589; MUID:90380278; PMID:2400579                                                                                                                                                                                                                                                                                                  |
| A; Once needs annotation with other gene products A; Note: comparison with other gene products C; Comment: Calpain I is activated by micromolar concentrations of calcium. C; Genetics: A; Gene: GDB:CAPNI; mu-CANP A; Cross-references: GDB:119749; OMIM:114220 A; Map position: 11pter-11qter C; Complex: heterodimer of L (large) and S (small) chains                                                                                                                                                                                                                                                                                                                                       |
| C.Function: A.Doce: cleaves preferentially after tyrosine, methionine, or arginine residues and befor A.Note: cleaves preferentially after tyrosine, methionine, or arginine residues and befor C.Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain C.Kewpords acetylated anno end; calcum binding; cysteine proteinase; duplication; EF P: 2-714/Product: calpain large chain I status predicted «MAT» F.2-10/Product: chemotactic factor #status experimental cHF» F.84-573/Domain: calpain catalytic domain homology <calp» <ef2»="" <ef2»<="" calmodulin="" domain:="" f.618-647="" f.668-617="" f.85-617="" homology="" repeat="" td=""></calp»>      |
| F;650-682/Domain: calmodulin repeat homology <ef5><br/>F;63-714/Domain: calmodulin repeat homology <ef5><br/>F;27/Modified site: acetylated amino end (Ser) (in mature form) #status experimental<br/>F;115,272,296/Active site: Cys, His, Asn #status predicted</ef5></ef5>                                                                                                                                                                                                                                                                                                                                                                                                                    |

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22; Conservative
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Best Local Similarity
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                                                                                                                                                            Calpain (EC 3.4.22.17) large chain 1 - chicken (fragment)

Nathernace names: mu-calpain heavy chain

C;Species: Gallus gallus (chicken)

C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

R;Sorimachi, H; Tsukahara, T; Okada-Ban, M; Sugita, H; Ishiura, S; Suzuki, K.

Biochim. Biophys. Acta 1261, 381-393, 1995

A;Title: Identification of a third ubiquitous calpain species - chicken muscle expresses

A;Reference number: S57194, MUID:95260862; PMID:7742367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:042133; EMBL:D38027; NID:9882070; PID:9882071
C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain
K;Keywords: cysteline proteinase; EF hand; hydrolase
F;1-208/Domain: calpain catalytic domain hydrology (fragment) <CALP>
F;457-489/Domain: calmodulin repeat homology <EF1>
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                                                   Gaps
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             Length 714;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 86.0%; Score 117; DB 2; Length 58 Local Similarity 85.7%; Pred. No. 8.6e-08; Als 24; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
           100.0%; Score 136; DB 1;
100.0%; Pred. No. 3.1e-10;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 2;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                       555 AGEDMEISVKELRTILNRIISKHKDLRT 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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Best Local Similarity 100.0
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps

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Best Loca Matches

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Calpain (EC 3.4.22.17) large chain 3 - chicken

N.Alecrnate names: calpain p94 heavy chain; n-calpain-1 heavy chain
C.Species: dallus gallus (chicken)
C.Species: dallus gallus (chicken)
C.Species: dallus gallus (chicken)
C.Species: lo-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S57196
R.Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzuki, K.
Biochim. Biophys. Acta 1261, 381-339, 1995
A;Title: Identification of a third ubiquitous calpain species - chicken muscle expresses
A;Tetle: Identification of a third ubiquitous calpain species - chicken muscle expresses
A;Tetle: Identification of a third ubiquitous calpain species
A;Accession: S57194, MUID:95260862; PMID:7742367
A;Accession: S57196
A;Status: preliminary
A;Accession: S57196
A;Status: preliminary
A;Coss-references: UNIPROT:Q92177; EMBL:D38028; NID:g882072; PIDN:BAA07230.1; PID:g15521
C;Superfamily: calpain large chain; calmodulin repeat homology <CALP>
F;746-778/Domain: calmodulin repeat homology <EFH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CiAccession: A00979
Richno, S.; Emori, Y.; Imajoh, S.; Kawasaki, H.; Kisaragi, M.; Suzuki, K.
Nature: 17.7371203 #Sequence_revision Of a calcium-dependent protease by fusion of genes for a thi Nature: Evolutionary Origin of a calcium-dependent protease by fusion of genes for a thi A; Reference number: A93148; MUD:85061606; PMID:6095110
A; Reference number: A93348; MUD:85061606; PMID:6095110
A; Residues: 1-705 < CHN>
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A; Residues: 1
                                                                                                                                                                                                                                                                                                               calpain (BC 3.4.22.17) large chain 4 - chicken
Albarian catalytic chain; intermediate calcium activated neutral protei
C;Species: Gallus gallus (chicken)
C;Date: 17-May-1985 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpescription: catalyzes the hydolysis of peptides
Alpescription: catalyzes the hydolysis of peptides
Alpescription: catalyzes the hydolysis of peptides
Cidaves preferentially after tyrosine, methionine, or arginine residues and befor
CiSuperfamily: calpain large chain; calmodulin repeat homology, calpain catalytic domain catalytic domain homology «EPI»
Figh.304 Domain: calpain catalytic domain homology «EPI»
Figh.304 Domain: calmodulin repeat homology «EPI»
Figh.304 Domain: calmodulin repeat homology «EPI»
Figh.305 Domain: calmodulin repeat homology «EFI»
Figh.40705/Domain: calmodulin repeat homology «EFI»
Figh.40705/Domain: calmodulin repeat homology «EFI»
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427 AGPDMEISVTELQTILNRITAKHKDLRT 454
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bovine (Species: Bos primigenius taurus (cattle) (Species: Bos primigenius taurus (cattle) (C)Species: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004 (C)Accession: A3446 (F) The Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of the Part of th
                                                                                                                                             A;Gene: GDB:CAPN3; CANP3; LGWD2A, LGMD2
A;Gene: GDB:CAPN3; CANP3; LGWD2A, LGMD2
A;Gene: GDB:CAPN3; CANP3; LGWD2A, LGMD2
A;Gene: GDB:L119751; OMIM:114240; OMIM:253600
A;Gene: GDB:L119751; OMIM:114240; OMIM:253600
A;Mote: defects in this gene can cause limb girdle muscular dystrophy 2A
A;Mote: defects in this gene can cause limb girdle muscular dystrophy 2A
C;Complex: heterodimer of L (large) and S (small) chains
C;Complex: heterodimer of L (large) and S (small) chains
C;Complex: heterodimer of L (large) and S (small) chains
C;Complex: defects in this gene can can gradulin repeat homology; capathonic calpain catalytic domain
C;Reywords: calcium binding; cysteine proteinase; EF hand; hydrolase; muscular dystrophy
C;Reywords: calcium binding; cysteine proteinase; EF hand; hydrolase; muscular dystrophy
F;69-267,323-400/Domain: calmodulin repeat homology <EF2>
F;725-739,Domain: calmodulin repeat homology <EF2>
F;725-739,Domain: calmodulin repeat homology <EF5>
F;725-739,Domain: calmodulin repeat homology <EF5>
F;726-738,Domain: calmodulin repeat homology <EF5>
F;726-738,Domain: calmodulin repeat homology <EF5>
F;729-334,358,Active site: Cys, His, Asn #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-dan-1995 #sequence_revision 06-dan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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      Molecule type: mRNA
;Residues: 44-445,'AA',448-458,'P',460-461,'P',463-484,'T',486-821 <SOR>
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Pred. No. 0.00014;
7; Mismatches 5; Indels
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66.9%; Score 91; DB 2; Length 184
Best Local Similarity 53.6%; Pred. No. 7.6e-05;
Matches 15; Conservative 8; Mismatches 5; Indels
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A,Accession: A34466
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 AGDDMEICADELKKVLNTVVNKHKDLKT 689
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Best Local Similarity 57.1%;
Matches 16; Conservative
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Bad488

calpain (EC 3.4.22.17) large chain 3 - rat

NiAlternate names: cysteine proteinase
Cyspecies: Ratus norvegicus (Norway rat)
Cyspecies: Ratus norvegicus (Norway rat)
Cyspecies: Ratus norvegicus (Norway rat)
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
Cybate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
Rysorimachi, H. Imajoh-Ohmi, S.; Emori, Y.; Kawasaki, H.; Ohno, S.; Minami, Y.; Suzuki,
A;Reference number: A94688; MulD:9062125; PMID:2555341
A;Recession: B34488
A;Molecule type: MRA
A;Residues: 1-81 -8208
A;Accession: B3468
A;Accession: SiDSB
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Calpain (EC 3.4.22.17) large chain 3 - human

Calpain (EC 3.4.22.17) large chain 3 - human

Calpain (EC 3.4.22.17) large chain 3 - human

NyAlternate names: calpain chain L-3; calpain III catalytic chain; muscle specific, calc

C; Species: Homo saptens (man)

C; Date: 28-Apr-1995 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C; Accession: A55218; A34488

R; Richard, I.; Broux, O.; Allamand, V.; Fougerousse, F.; Chiannilkulchai, N.; Bourg, N.;

J.A.; Fardeau, M.; Jackson, C.E.; Cohen, D.; Beckmann, J.S.

Cell 81, 27-40, 1995

A; Title: Mutations in the protecolytic enzyme calpain 3 cause limb-girdle muscular dystrc

A; Reference number: A56218; MUID:95236448; PMID:7720071

A; Reference number: A56218; MUID:95236448; PMID:7720071

A; Reference number: A56218

A; Reference number: Bail (RIC)

A; Reference number: Bail (RIC)

A; Reference number: Bail (RIC)

A; Cross-references: UNIPROT:P20807; GB:X85030; NID:9791039; PIDN:CAA59403.1; PID:9791046

R; Sorimachi, H.; Imajoh-Ohmi, S.; Emori, Y.; Kawasaki, H.; Ohno, S.; Minami, Y.; Suzuki,
J. Biol. Chem. 264, 20106-20111, 1989

A; Title: Molecular cloning of a novel mammalian calcium-dependent protease distinct from A; Reference number: A34488

A; Reference number: A34488
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      Length 810;
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                                                                                                                    5; Indels
Score 97; DB 1; 1
Pred. No. 5.5e-05;
6; Mismatches 5;
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      Query Match
Best Local Similarity 60.7%;
Matches 17; Conservative
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hes 16; Conservative
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A, Cross-references: VINPROT: P06813; GB:M13364; NID:g164875; PIDN:AAA81565.1; PID:g164876 C; Complex: heterodimer of L (large) and S (small) chains
C; Complex: heterodimer of L (large) and S (small) chains
C; Function:
A; Description: catalyzes the hydolysis of peptides
A; Description: catalyzes the hydolysis of peptides
A; Description: catalyzes the hydolysis of peptides
A; Note: cleaves preferentially after tyrosine, methionine, or arginine residues and before; Superfamily: calpain small chain; calmodulin repeat homology
F; H= 154 Domain: calmodulin repeat homology ceFt>
F; 154 Domain: calmodulin repeat homology ceFt>
F; 202-234 Domain: calmodulin repeat homology ceFt>
F; 202-234 Domain: calmodulin repeat homology ceFt>
F; 202-234 Domain: calmodulin repeat homology ceFt>
F; 202-234 Domain: calmodulin repeat homology ceFt>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
R;Miyake, S:; Emori, Y:; Suzuki, K.
Nucleic Acids Res. 14, 8805-8817, 1986
A;Title: Gene organization of the small subunit of human calcium-activated neutral protective and accession: A20107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P04632; GB:M31502
R;Ohno, S.; Emori, Y.; Suzuki, K.
N;Otleic Acids Res. 14, 5559; 1986
A;Title: Nucleotide sequence of a cDNA coding for the small subunit of human calcium-depc
A;Reference number: A93631; MUID:B6286563; PMID:3016651
A;Accession: A23650
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A;Residues: 1-268 <OHN>
A;Cross-references: EMBL:XO4106; NID:g35327; PIDN:CAA27726.1; PID:g35328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calpain (EC 3.4.22.17) small chain - human N;Alternate names: calcium-activated neutral proteinase (CANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.9%; Score 91; DB 1; Lei
53.6%; Pred. No. 0.00011;
Miematches 5;
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53.6%; Pred. No. 0.00011;
ive 8; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AGDDMEVSATELMNILNKVVTRHPDLKT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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Best Local Similarity 53.6
Matches 15; Conservative
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                             A; Residues: 1-266 < EMO>
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A;Residues: 1-268 <MIY>
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Best Local Similarity
Matches 15; Conserv
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F; 94-125/Domain: calmodulin repeat homology <EF!>
                      A.Cross-references: UNIPROT: P13135, GB:J05065; NID:g162780; PIDN:AAA30422.1; PID:g162781
C.Superfamily: calpain small chain; calmodulin repeat homology
C.Superfamily: calpain small chain; calmodulin repeat homology
E.Superfamily: calpain banding; cysteine proteinase; duplication; EF hand; heterodimer; hyd
F:J1-51/Domain: glycine-rich cGLY>
F:J1-51/Domain: calmodulin repeat homology cEF1>
F:J34-166/Domain: calmodulin repeat homology cEF3>
F:J99-231/Domain: calmodulin repeat homology cEF4>
F:J99-231/Domain: calmodulin repeat homology cEF5>
F:J32-263/Domain: calmodulin repeat homology cEF5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calpain (EC 3.4.22.17) small chain - pig

NA Alecarate names calculan-activated neutral proteinase (CANP); calpain light chain; cal

C,Alecarate names calculan-activated neutral proteinase (CANP); calpain light chain; cal

C,Species: Sus scrofa domestica (domestic pig)

C,Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C,Accession: A25166; B25166

R,Sakihama T.; Kakidani, H.; Zenita, K.; Yumoto, N.; Kikuchi, T.; Sasaki, T.; Kannagi, Proc. Natl. Acad. Sci. U.S.A. 82, 6075-6079, 1985

A,Title: A putative Ca2+-binding protein: structure of the light subunit of porcine calp

A,Reference number: A25166; MUID:85298299; PMID:2994060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P04574; GB:M11778; NID:g164402; PIDN:AAA31010.1; PID:g164403
Accession: B25166
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N;Alternate names: calcium-activated neutral proteinase (CANP); calpain light chain; cal
S;Species orycrolagus cuniculus (domestic rabbit)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24816
R;Emori, Y.; Kawasaki, H.; Imajoh, S.; Kawashima, S.; Suzuki, K.
A;Eiol. Chem. 261, 9472-9476, 1986
A;Title: Isolation and sequence analysis of cDNA clones for the small subunit of rabbit
A;Reference number: A24816; MUID:86250903; PMID:3013892
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F;137-166/Domain: calmodulin repeat homology <EF2>
F;170-199/Domain: calmodulin repeat homology <EF3>
F;202-234/Domain: calmodulin repeat homology <EF4>
F;235-266/Domain: calmodulin repeat homology <EF5>
F;235-266/Domain: calmodulin repeat homology <EF5>
F;1/Modified site: acetylated amino end (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                Length 263;
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Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
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Residues: 2-56;125-143;157-177;247-248;250-256;265-266
Complex: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                            Score 91; DB 2; I
Pred. No. 0.00011;
8; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AGDDMEVSATELMNILNKVVTRHPDLKT 131
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53.6%;
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Best Local Similarity 53.6
Matches 15; Conservative
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Best Local Similarity
A;Residues: 1-263 <MCC>
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Residues: 1-266 <SAK>
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A Description: catalyzes the hydolysis of peptides
A Note: cleaves preferentially after tyrosine, methionine, or arginine residues and befor
C;Superfamily: calpain small chain, calmodulin repeat homology
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hydr.
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hydr.
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hydr.
C;Keywords: calcium binding; cysteine proteinase; duplication; EF P;137/Domain: calmodulin repeat homology <EF2>
F;237-268/Domain: calmodulin repeat homology <EF5>
F;237-268/Domain: calmodulin repeat homology <EF5>
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A, Cross-references: GDB:119752; OMIN:114170
A, Map position: 19pter-19qrer
A; Introns: 70/2; 81/3; 111/3; 131/1; 152/3; 175/3; 202/1; 241/1; 260/3
C; Complex: heterodimer of L (large) and S (small) chains
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AGDDMEVSATELMNILNKVVTRHPDLKT 136

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264 AGEDAEISAFELQNILRRVLAKRODIKT 291
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Matches
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CHINGE 3.4.2.17) large chain 2 - human
Nathernate names: calaplain chain 1-3; calpain in catalytic chain, high-calcium requiring
Chaccasine and ansers calablain chain L-3; calpain in catalytic chain, high-calcium requiring
Chaccasine and ansers calablain chain L-3; calpain in catalytic chain, high-calcium requiring
Chaccasine and ansers calablain chain L-3; calpain in catalytic chain, high-calcium requiring
Chaccasine and ansers calabrain chain L-3; calpain in catalytic chain, high-calcium requiring
Richarden and Chaccasine and Chain and Chain and Chaccasine and Chaccasine and Chaccasine and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain and Chain a
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S38361
calpain (EC 3.4.22.17) II large chain - rat
NyAlternate names: calpain II 80% chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S38361, S08565, $39751
R;DeLuca, C.I.; Davies, P.L.; Samis, J.A.; Elce, J.S.
Biochim: Biophys. Acta 1216, 81-93, 1993
A;Title: Molecular cloning and bacterial expression of cDNA for rat calpain II 80 kDa
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Pred. No. 0.0063;
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8; Mismatches
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ilarity 53.6%;
Conservative 6
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Best Local Similarity
Matches 15; Conserv
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A,Molecule type: mRNA
A,Residuss: 1-700 <DEL>
A,Residuss: 1-700 <DEL>
A,Residuss: 1-700 <DEL>
A,Samis, Jo.A.; Back, D.W.; Graham, E.J.; Elice, J.S.
submitted to the EMBL Data Library, February 1990
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A.Rocession: 80850
A.Accession: 80850
A.Accession: 80850
A.Residues: 380-439 csAN
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Reference number: S38361; MUID:94032492; PMID:8218419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGEDMEISVKELRTILNRIISKHKDLRT 28
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542 AGEDAEISAFELQTILRRVLAKREDIKS 569

C)Accession: B24815.
F. Kawashima, B.; Sugihara, H.; Imajoh, S.; Kawashima, S.; Suzuki, K.
J. Biol. Chem. 261, 9465-9471, 1986
A)Title: Isolation and sequence analyses of cDNA clones for the large subunits of two isc
A)Reference number: A92594; WUID:86250902; PMID:2424911 C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 24-Jan-1988 #sequence\_revision 24-Jan-1988 #text\_change 09-Jul-2004 calpain (EC 3.4.22.17) large chain 2 - rabbit (fragment) N/Alternate names: calcium-activated neutral proteinase (CANP)

A; Accession: B24815
A; Molecule type: mRNA
A; Residues: 1-42 < EMOA; Cross-references: 1-42 < EMOA; Cross-references: 1-422 < EMOC; Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain C; Keywords: calcium binding; cysteine proteinase; EF hand; hydrolase
F; 521-282, Domain: calmodulin repeat homology < EF1F; 294-326, Domain: calmodulin repeat homology < EF2F; 327-356, Domain: calmodulin repeat homology < EF2F; 327-356, Domain: calmodulin repeat homology < EF2F; 359-391, Domain: calmodulin repeat homology < EF3-Length 422;

Gaps . 0 6; Indels Query Match 58.8%; Score 80; DB 2; Best Local Similarity 53.6%; Pred. No. 0.0052; Matches 15; Conservative 7; Mismatches

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gallus gall

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0862h4 mus musculu
Bad16622 mus musculu
Bad16622 mus musculu
008702 rattus morv
070482 rattus morv
046491 mus musculu
p16259 rattus morv
071470 homo sapien
Bad1649 homo sapien
Bad1649 homo sapien
099197 macaca fasc
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01-APR-1988 (Rel. 07, Last sequence update)
05-UDL-2004 (Rel. 44, Last annocation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
Name=CAPN1; Synonyms=CANPL1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Calpain 1 (Fragment).
Ovis arres (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Busaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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CAN3_RAT
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  CHICK
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BAD16652
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BAD16649
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070482
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    Local Similarity 100.
Les 28; Conservative
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Q9GL55;
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CAN1 HUMAN
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06dhv4 homo sapien

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090185 bos taurus

0900m7 sus scrofa

03550 sus musculu

08021 rattus norv

080271 rattus norv

080271 mus musculu

08021 mus musculu

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08021 cattus no

07081 cartus no

07089 gallus gall

07089 gallus gall

09091 coturnix co

06paf2 xenopus lae

072xx1 brachydanio

091802 brachydanio

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072xq4 xenopus lae

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Ossil sus scrofa
P43368 sus scrofa
P51186 bos taurus
O9tth8 ovis aries
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                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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CAN1_HUMAN
CAN1_MACFA
Q6DHV4
CAN1_BOVIN
Q9N18S
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CAN1_MOUSE
CAN1_RAT
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CAN3_PIG
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CAN3_SHEEP
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Gaps

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GO; GO: 0008284; P:positive regulation of cell proliferation; TAS.

InterPro; IPR0103048; EF-hand.

InterPro; IPR0103048; EF-hand.

InterPro; IPR0103049; EF-Hand. Like.

InterPro; IPR001309; Peptidase_C2.

InterPro; IPR001309; Peptidase_C2;

InterPro; IPR001309; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

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InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; Peptidase_C2;

InterPro; IPR00130; IPR00130; INTERPRO;

IPR00117; PR00130; IPR00130;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
10-0CT-2004 (Rel. 44, Last annotation update)
10-0CT-2004 (Rel. 44, Last annotation update)
10-0CT-2004 (Rel. 44, Last annotation)
10-0CT-2014 (Rel. 44, Last annotation)
10-0CT-2014 (Micromolar Calpain)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
By similarity.
By similarity.
K -> N (in Ref. 3; AAHOB751).
ICBGD7C56D063498 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355
527
527
528
628
663
663
1115
1115
272
272
248
548
514
714 AA;
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SEQUENCE FROM N.A.
TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9541;
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ACT_SITE
ACT_SITE
CONFLICT
SEQUENCE
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ID CANI MAC
AC Q9GLG2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca(2+) binding (By similarity).

- membrane upon Ca(2+) binding (By similarity).

- TISSUE SPECIFICITY: Ubiquitous family C2.

- SIMILARITY: Belongs to peptidase family C2.

- SIMILARITY: Contains 1 Calpain catalytic domain.

- SIMILARITY: Contains 2 EP-hand calcium-binding domains.

- DATABASE: NAME=CaBP; NOTE=Calpain;

WWW="http://arucbio.vanderbilit.edu/cabp_database/general/prot_pages/calpain.h

- DATABASE: NAME=Calpains homepage;

WWW="http://ag.arizona.edu/calpains".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Kidney, and Placenta;

XX TISSUB-Kidney, and Placenta;

XX TISSUB-Kidney, and Placenta;

XX TISSUB-Kidney, and Placenta;

XX TISSUB-Kidney, and Placenta;

XX TISSUB-Kidney, and Placenta;

XX TISSUB-XID TIS, Wadger L., Bremen C.M., Schuler G.D.,

XX TISSUB-XID, Colling F.S., Wadger L., Shemen C.M., Schuler G.D.,

XX TISCHOL S. F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Tapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Worley Y.C., Hale S., Garcia A.M., Gunaratne P.H.,

XX Richards S., Worley V.M., Sodesgren B.J., Lu X., Ginbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodesgren B.J., Lu X., Gibbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodesgren B.J., Lu X., Gibbs R.A.,

XX Hilalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XX Hilalon B., Young A.C., Shevchenko Y., Bouffaud G.G.,

XX Radriquez A.C. Grimwood J., Schmutz J., Myers R.M.

XX Schein J.B., Schmitz J., Skalska U., Smailus D.E.,

XX Scherztield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Bronezth A., Schein J.E., Jones B.J.M., Marra M.A.,

XX A. Marra M.A.;

XX A. Marra M.A.;

XX A. Marra M.A.;

XX A. Marra M.A.;

XX A. Marra M.A.;

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XX A. Mar
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                  MEDLINE-86301172; PubMed=3017764;
Aoki K., Imajoh S., Ohno S., Emori Y., Koike M., Kosaki G., Suzuki K.;
"Complete amino acid sequence of the large subunit of the low-Ca2+-
requiring form of human Ca2+-activated neutral protease (muCANP)
deduced from its cDNA sequence.";
FEBS Lett. 205:313-317(1986).
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-90380278; PubMed-2400579;
Sorimachi H., Ohmi S., Emori Y., Kawasaki H., Saido T.C., Ohno S.,
Minami Y., Suzuki K.;
Minami Y., Suzuki K.;
Minami Y., Suzuki K.;
Minami Y., Suzuki K.;
Minami Y., Suzuki K.;
Minami Y., Suzuki K.;
Minami Y., Saido T.C., Ohno S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyzes limited proteolysis of substrates involved in cytoskeletal remodelling and signal transduction.

-!- CATALYTIC ACTIVITY: Broad endopeptidase specificity.
-!- COPACTOR: Binds 3 calcium ions.
-!- COPACTOR: Binds Activated by micromolar concentrations of calcium and inhibited by calpastatin.
-!- SUBUNTI: Forms a heterodimer with a small (regulatory) subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC008751; AAH08751;
EMBL; BC017200; AAH17200.1;
PIR, AA5213; CHUH.
HSSP; P97511; IKXR.
MEROPS; C02.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X04366; CAA27881.1; -.
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Genew; HGNC:1476; CAPN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Richards R.D., Feligold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Repleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McZwan P.U., McKernan K.J., Mallek J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rachiquez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANI BOVIN STANDARD; PRT; 716 AA.
027970; QSNOV6;
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-CCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last sequence update)
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Sun W., Bidwell C.A., Ji S., Hancock D.L.;

Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

-!- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

-!- CATALYTIC Binds 3 calcium ions.

-!- ENZYME REGULATION: Activated by micromolar concentrations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20500419; PubMed=11048924;
Smith T.P.L., Casas E., Rexroad C.E. III, Kappes S.M., Keele J.W.,
Bovine CAPNI maps to a region of BTA29 containing a quantitative
trait locus for meat tenderness.";
J. Anim. Sci. 78:2589-2594(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078862; AAH78862.1; -.
GEOTIENCE 714 AA; 81830 MW; 46B6556D4707428F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 136; DB 2;
100.0%; Pred. No. 2.5e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                   MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 530-625 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pancreas;
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CAN1_BOVIN
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                  Cytoplasmic; Translocates to the plasma ding (By similarity).
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Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain IV.
Ancestral calcium site 1 (Potential)
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PROSITE; PS0203; CALPAIN_CAT; 1.

PROSITE; PS000018; EF HAND; 2.

PROSITE; PS00640; THIOL_PROTEASE ASN; FALSE_NEG.

PROSITE; PS006139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE NEG.

Calcium-binding; Hydrolase; Multigene family; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 136; DB 1; Length 714; 100.0%; Pred. No. 2.5e-09;
      SUBCELLUTAR LOCATION: Cytoplasmic; Translocates to the membrane upon Ca++ binding (By similarity).
TISSUE SPECIFICITY: Ubdilitous.
SIMILARITY: Belongs to peptidase family C2.
SIMILARITY: Contains 1 Calpain catalytic domain.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Last annotation update)
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Ancestral calcium
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By similarity.
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InterPro; IPR010983; EF-Hand like.
InterPro; IPR010983; EF-Hand like.
InterPro; IPR001300; Peptidase_C2.
InterPro; IPR00169; Pept Cys_acsite.
Pfam; PF001067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN_
SWART; SW00230; CyePc; 1.
SWART; SW000230; CyePc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF-hand 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF284440; AAG22770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81849 MW;
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01-OCT-2004 (TrEMBLrel. 28,
01-OCT-2004 (TrEMBLrel. 28,
CAPNI protein.
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272
296
296
714 AA;
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hes 28; Conserv
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DOMAIN 55
DOMAIN 355
DOMAIN 543
DOMAIN 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; C02.
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ACT_SITE
ACT_SITE
SEQUENCE
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Matches

RESULT 4

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Gaps

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Length 714; Indela

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NEOLINE=21087425; PubMed=11219468; MEDLINE=21087425; PubMed=11219468; Smith T.P.L., Simmen F.A., Zhao G., Vallet J.L.; Simmen F.A., Zhao G., Vallet J.L.; Simmen F.A., Zhao G., Vallet J.L.; Simmen F.A., Zhao G., Vallet J.L.; Simmen F.A., Zhao G., Vallet J.C.; Simmen F.A., Zhao G., Vallet J.C.; Simmen F.A., Zhao G., Vallet J.C.; Simmen F.A., Zhao G., 79:552-553 (2001).
HSSP, P97571; IKXR.
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O9NON7

O9NON7

O9NON7

O9NON7

O1-OCT-2000 (TrEMBIrel. 15, Last sequence update)

O1-OCT-2000 (TrEMBIrel. 26, Last annotation update)

O1-MAR-2004 (TrEMBIrel. 26, Last annotation update)

Micromolar calcium-activated neutral protease 1 isoform B.

Sus scrofa (Pig)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                           Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                            Smith T.P.L., Gasas B., Rexroad C.E., Kappes S.M., Keele J.W.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AR221129; ARF32364.1; -. PIR; S16181; S16181.
                                                                                                                                                                                                                                                                                                                                                                                               Habsi P9/3715 Takar.

GO; GO:0005502; C:intracellular; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004198; F:calcium ion binding; IEA.

GO; GO:0006233; F:peptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001089; EF.hand.

InterPro; IPR001089; EF.hand.

InterPro; IPR001099; EF. Hand.

InterPro; CRO01300; Peptidase_C2.

InterPro; CRO01301; Peptidase_C2.

Pfam; PF01067; Calpain_III; 1.

Pfam; PF00056; efhand; 3.

Pfam; PF00548; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716 AA; 82207 MW; A7F55C197BD5DF23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; 600:005622; C:intracellular; IEA.
GO; GO:0005629; F:calcium ion binding; IEA.
GO; GO:0008293; F:calpain activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002048; EF-hand.
InterPro; IPR010300; Peptidase_C2.
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100.0%; Pred. No. 2.5e-09;
iive 0; Mismatches 0;
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PROSITE; PSC0018; EF_HAND; UNKNOWN_2.
PROSITE; PSC0139; THIOL_PROTEASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGEDMEISVKELRTILNRIISKHKDLRT 28
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SMART; SM00720; Calpain III; 1.
SMART; SM000230; CysPC; I.
SWART; SM00054; EPh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9913;
Name=CAPN1;
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Q9NOM7
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                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R PROSITE; PS500203; CALPAND, 2.

R PROSITE; PS000189; THIOL_PROTEASE ASN; FALSE_NEG.

R PROSITE; PS000640; THIOL_PROTEASE_CYS); FALSE_NEG.

R PROSITE; PS000639; THIOL_PROTEASE_CYS); FALSE_NEG.

R PROSITE; PS000639; THIOL_PROTEASE_CYS, FALSE_NEG.

R PROSITE; PS000639; THIOL_PROTEASE_HIS; PALSE_NEG.

T DOMAIN 55 324 Calpain catalytic.

DOMAIN 529 544 Domain II.

T DOMAIN 556 567 BF-hand 2 (By similarity).

T CA_BIND 600 611 EF-hand 2 (By similarity).

T CA_BIND 600 641 EF-hand 2 (By similarity).

T DOMAIN 665 676 Ancestral calcium site 5 (Potential).

R OCHAIN 665 706 Ancestral calcium site 5 (Potential).

R ACT_SITE 272 272 By similarity.

I ACT_SITE 296 296 By similarity.

I ACT_SITE 296 296 By similarity.

I CONFILCT 530 530 V -> I (in Ref. 2).
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calcium and inhibited by calpastatin.

-!- SUBUNIT: Heterodimer of a large (catalytic) and a small (regulatory) subunit.

-!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca++ binding (By similarity).

-!- SIMILARITY: Belongs to peptidase family C2.

-!- SIMILARITY: Contains 2 EP-hand calcium-binding domains.

-!- CAUTION: Ref. 2 sequence differs from that shown due to a frameshifts in positions 582 and 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-ON-AR-2004 (TrEMBLrel. 26, Last annotation update)
Micromolar calculun-dependent neutral protease large subunit.
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-> A (in Ref. 2).
8FFD61331DAB8AD5 CRC64;
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100.0%; Pred. No. 2.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR002048; BF-hand.
Interpro: IPR001300; Peptidase C2.
Interpro: IPR001300; Peptidase C2.
Fram; PF001067; Calpain_III; 1.
Fram; PF001067; Efhand, 3.
Fram; PF001064; Efhand, 3.
Fram; PF001049; Peptidase C2; 1.
PRINTS; PR00704; CALPAIN.
SWART; SW00720; CAPEC; I.
SWART; SW00220; CyEPC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF248054; AAF64504.2; -.
EMBL, AF252504; AAF64504.2; JOINED.
EMBL; U07849; AAA18454.1; ALT_FRAME.
PIR; S16181; S16181.
MHSSP, P17655; IRFU.
MEROPS; C02.001; -.
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es 28; Conservative
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Q9N185;
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RESULT 6
Q9N185
ID Q9N1
AC Q9N1
DT 01-0
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Gaps

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Length 716; Indels

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SWISS-PROT entry is copyright. It is produced through a collaboration
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96.4%; Pred. No. 6.2e-09;
iive 1; Mismatches 0
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Domain IV.
                                                                                                                                                                                                                                                                                         EMBL; AF263610; AAF73444.1; -.
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                                                                                                                                                                                                                                                                                                                       EMBL; F14611; CAA23154.1; -. EMBL; U01180; AAA65125.1; -. HSSP; P97571; IKXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.4%;
Matches 27; Conservative
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528
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; C02.001;
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X MEDLINE=94146155; PubMed=8312396;
A MEDLINE=94146155; PubMed=8312396;
Sun W. Ji S.Q., Ebert P.J., Bidwell C.A., Hancock D.L.;
Sun W. Ji S.Q., Ebert P.J., Bidwell C.A., Hancock D.L.;

X Keletal muscle.";
Biochimie 75:931-936(1993)

- !- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

- !- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- !- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

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- !- CATALYTIC ACTIVITY: Broad endopeptidase specificity.
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P35750; Q29600; Q9NOM6;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Calpain 1, large [catalytic] subunit (BC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 porcine
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TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: Belongs to peptidase family C2.
SIMILARITY: Contains 1 Calpain catalytic domain.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
97.8%; Score 133; DB 2; Length 65
Best Local Similarity 96.4%; Pred. No. 5.7e-09;
Matches 27; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                650 AA; 74033 MW; 2EFE9FF569D90FD7 CRC64;
InterPro; IPR000169; Pept_cys_acsite.
Pfam; PF001067; Calpain_III; 1.
Pfam; PF001036; edhand; 2.
Pfam; PF001036; edhand; 2.
Pfam; PF00104; Calpain_III; 1.
SMART; SM00720; Calpain_III; 1.
SMART; SM00720; Calpain_III; 1.
SMART; SM00054; EFh; 2.
PROSITE; PS0203; CALPAIN_CAT; 1.
PROSITE; PS001039; THIOL_PROFEASE_CYS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANI MOUSE STANDARD; PRT; 713 AA.
035350, 088668 (1)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
neutral proceinase) (CANP) (Mu-type) (MucANP) (Micromolar-calpain).
Name-Capal; Synonyms-Canpl, Capal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poirier C., Poussard S., Faust D.M., Imaizumi-Sherrer T., Weiss M.C., Ducastaing A., Montarras D., Pinset C., Guenet J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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EF-hand 2.
EF-hand 3.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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--- 0; Indels
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Ancestral calcium site 5 (P
By similarity.
By similarity.
V -> I (in Ref. 3).
I -> N (in Ref. 3).
E -> G (in Ref. 3).
S -> A (in Ref. 3).
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CAN1 RAT P97571;
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ACT_SITE
ACT_SITE
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                                                                                                         Sahr K.E., Andrabi S., Peters L.L., Chishti A.H.; "Cloning and characterization of the cDNA and gene encoding the mouse mu-calpain large subunit protein."; submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";

1. Converse and integrated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

1. CATALYTIC ACTIVITY: Broad endopeptidase specificity.

1. COFACTOR: Binds 3 calcium ions (By similarity).

1. ENZYME REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpastentin.

2. SUBUNIT: Forms a heterodimer with a small (regulatory) subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca(2+) binding (By similarity).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to peptidase family C2.
-!- SIMILARITY: Contains 1 calpain catalytic domain.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF021847, AAB72222.1; -.
EMBL, AF084459; AAC33134.1; -.
EMBL, BC026138; AAH26138.1; -.
HSSP, P97571; IKXR.
MEROPS; C02.001; -.
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SMART; SM00230; CysPc; 1.
                                                                                                                                                                                                                                                                                  STRAIN=FVB/N; TISSUE=Colon;
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                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       FROM N.A
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Calpain 1, large (catalytic) subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
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**REDLINE=97107433; PubMed=89501733;

**REDLINE=97107433; PubMed=89501733;

**REDLINE=97107433; PubMed=89501733;

**REDLINE=97107433; PubMed=89501733;

T **Primary sequences of rat mu-calpain large and small subunits are, respectively, moderately and highly similar to those of human.";

**Elechim. Biochys. Acta 1309:37-41(1996)

- Catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- CATALYTIC ACTIVITY: Broad endopeptidase specificity.

- CATALYTIC FOTTON: Activated by mirromolar concentrations of calcium and inhibited by calpastatin.

- SUBDNIT: Forms a heterodimer with a small (regulatory) subunit
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancestral calcium site 4 (Potential).
Ancestral calcium site 5 (Potential).
By similarity.
By similarity.
L > P (in Ref. 2).
D -> N (in Ref. 2).
W, 3E1E26C95802B864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Ancestral calcium site 1 (Potential).
EF-hand 2.
EF-hand 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLUIAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca(2+) binding (By similarity).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to peptidase family C2.
-!- SIMILARITY: Contains 1 Calpain catalytic domain.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                      Thiol protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%; Score 129; DB 1; Length 713; 92.9%; Pred. No. 2.1e-08; ive 2; Mismatches 0; Indels
PROSITE; PS50203; CAUFALL.

R PROSITE; PS00018; EF HAND; 2.

R PROSITE; PS00139; THIOL PROTEASE CYS; 1.

R PROSITE; PS00139; THIOL PROTEASE TYS; FALSE NEG.

R PROSITE; PS006139; THIOL PROTEASE HIS; FALSE NEG.

RW Calcium-binding; Hydrolase; Multigene family; Thiol

FT DOMAIN 355 525 Domain III.

PT DOMAIN 355 525 Domain III.

PT DOMAIN 256 541 Linker.

712 Domain IV.
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Rattus norvegicus (Rat).
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Matches 26; Conserv
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STRAIN=FVB/N; TISSUE=Salivary gland;
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24,
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Mus musculus (Mouse).
                                                                               319
333
338
347
713 AA;
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Best Local Similarity
Matches 26; Conserv
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Name=Capnl;
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                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                           Ancestral calcium site 1 (Potential).
EF-hand 2.
EF-hand 3.
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                                                                                                             PROSTIE: PSCOOLS; CALPAIN CAT; 1.
PROSTIE: PSCOOLS; EF HAND, 2.
PROSTIE: PSCOOLS; THIOL. PROTEASE ASN; FALSE_NEG.
PROSTIE: PSCOOLS; THIOL. PROTEASE CYS; 1.
PROSTIE; PSCOOLS; THIOL. PROTEASE CYS; 1.
PROSTIE; PSCOOLS; THIOL. PROTEASE THIS; FALSE NEG.
DOMAIN
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DOMAIN III.
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Ancestral calcium site 5 (18 sy similarity.
By similarity.
By similarity.
                                                                                                                                                                 Linker.
Domain IV.
                      PDB; 1KKR; X-ray; A/B=26.364.

MEROPS; CO2.01; -AB=26.364.

MEROPS; CO2.01; -AB=26.364.

InterPro; Capn1.

InterPro; IPR010983; EF Hand like.

InterPro; IPR001300; Peptidase_C2.

InterPro; IPR001300; Peptidase_C2.

InterPro; IPR00169; Peptidase_C2.

Pfam; PF001067; Calpain_III; 1.

Pfam; PF000648; Peptidase_C2; PRINTS; PR00704; CALPAIN_C3.

PRINTS; PR00704; CALPAIN_C3.

SMART; SM007030; CAPEC; I.

SMART; SM00230; CAPEC; I.
                  EMBL; U53858; AAC53001.1;
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SEQUENCE FROM N.A.

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SEQUENCE 238825; PubMed=1247932;

MEDLINE=2238825; PubMed=1247932;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                               Length 713;
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352
82118 MW; 6E664600B0EFABBB CRC64;
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Last sequence update)
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                                                                                                                                               94.9%; Score 129; DB 1;
llarity 92.9%; Pred. No. 2.1e-08;
Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      713 AA
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Local Similarity 92.9
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AAH61880;
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02-MAR-2004 (
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STRAIN=NOD; TISSUE=Thymus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=2049374; Pubmed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:E430019P14 product:calpain 1, full
insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.9%; Score 129; DB 2; Length 713; 92.9%; Pred. No. 2.1e-08; ive 2; Mismatches 0; Indels
R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0004198; F:calcium ion binding; IEA.

R GO; GO:0004198; F:calcium ion binding; IEA.

GO; GO:0004198; F:calcium ion binding; IEA.

GO; GO:0004198; F:calcium ion binding; IEA.

InterPro; IPRO02048; EF-hand.

InterPro; IPRO01300; Peptidase_C2.

InterPro; IPRO01300; Peptidase_C2.

InterPro; IPRO0169; Pepti Cys_acite.

R Ffam; PF00046; Peptidase_C2; I.

R Ffam; PF00049; Peptidase_C2; I.

R PRONTS; PR00704; CALPAIN.

R PROMINS; RN00120; CALPAIN.

R SWART; SN00120; CALPAIN.

R SWART; SN00120; CALPAIN.

R SWART; SN00121; BF-hand; I.

R SWART; SN00139; CALPAIN CAT; I.

R SWART; SN00139; CALPAIN CAT; I.

R PROSITE; PS0203; CALPAIN CAT; I.

R PROSITE; PS0203; CALPAIN CAT; I.

R PROSITE; PS00108; BF HAND, UNKNOWN 2.

R PROSITE; PS00108; BF HAND, UNKNOWN 2.

R PROSITE; PS00108; BF HAND, PROTEASE CYS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 AGDDMEISVKELQTILNRIISKHKDLRT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NOD; TISSUB=Thymus;
BEDLINES=29279253; PubMed=1349636;
Carninci P., Hayabhizaki Y.;
"High-efficiency full-length cDNA '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 92.9
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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C STRAIN-NOD, TISSUE-Thymus,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A hayashida K., Hayatsu W., Harangaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu I., Hiramoto K., Hiroka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Kondo Y., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno W., Ohsato N., Okazaki Y.,
A saito R., Saitoh H., Sakai C., Sakai K., Sasatume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (ApR-2002) to the EMBL/GenBank/DDBJ databases.
BENEL, AKO88647; BAC40416.1; -.
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"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STARLIN-BODD, TISSUE-Thymus;

MEDLINE-20530913; PubMed-11076861;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Konnon H., Akiyama J., Nahai K., Kitsuama T., Tashiro H., Itoh M.,

A Wamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Pujwake S., Inoue K., Togawa W., Izanawa M., Ohara E., Watahiki M.,

A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated Sequence analysis (RISA) System-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:88263; Capn1.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:000503; F:calcium ion binding; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR0105048; EF-hand.
InterPro; IPR0105048; EF-hand.
InterPro; IPR0105049; EF-hand.
InterPro; IPR0105049; Peptidase_C2.
InterPro; IPR0105093; Pept cyg_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00648; Peptidase_C2: 1.
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ProDom; PD00012; EF-hand; 1.

SMART; SM00720; Calpain_III; 1.

SMART; SM00024; EFh; 3.

SMART; SM00054; EFh; 3.

PROSITE; PS50019; EF HAND; UNKNOWN 2.

PROSITE; PS00019; FF HAND; UNKNOWN 2.

SEQUENCE 713 AA; 82152 MW; 3EIFCB4D5802864 CRC64;
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(TremBlrel. 27, Last sequence update)
(TremBlrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.9%; Score 129; DB 2; 92.9%; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 AA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 -I- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
-!- CATALYTIC ACTIVITY: Broad endopeptidase specificity.
-!- COFACTOR: Binds 3 calcium ions (By similarity).
-!- BNZNMR REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpastatin.
-!- SUBENIT: Forms a heterodimer with a small (regulatory) subunit
                                                                                                                                                                                                                                                                      -1-SUBCELLUIAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca(2+) binding (By similarity).
-1-TISSUE SPECIFICITY: Ubjultous.
-1-SIMILARITY: Belongs to peptidase family C2.
-1-SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain IV.
Ancestral calcium site 1 (Potential)
EF-hand 2.
EF-hand 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ancestral calcium site 4 (Potential)
Ancestral calcium site 5 (Potential)
178BFEF4216C6EAB CRC64;
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-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein zgc:63788.
Mame=zgc:63788,
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata, Cranlata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002048; EF-hand 1. Re InterPro; IPR002048; EF-hand 1. Re InterPro; IPR001300; Peptidage C2.

R InterPro; IPR001300; Peptidage C2.

R InterPro; IPR00169; Peptidage C3.

R PEAM; PF00167; Calpain_III; 1.

R SMART; SM00526; efhand; 3.

R SMART; SM00526; EFH; 3.

R PROSITE; PS00640; THĪOL_PROTEASE ASN; PARTIAL.

R PROSITE; PS00639; THIOL_PROTEASE CYS; PARTIAL.

R PROSITE; PS0639; THIOL_PROTEASE HIS; PARTIAL.

R PROSITE; PS0639; THIOL_PROTEASE HIS; PARTIAL.

R PROSITE; PS0639; THIOL_PROTEASE HIS; PARTIAL.

R PROSITE; PS0639; THIOL_PROTEASE HIS; PARTIAL.

R PROSITE; PS0639; THIOL_PROTEASE HIS; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1e-07;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                          can bind Ca2+ ions."; them. 101:889-895(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M13363; AAA31456.1; -. PIR; A24815; A24815.
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Best Local Similarity 85.7%;
Matches 24; Conservative
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130
153
153
262
262
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MEROPS; C02.001;
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SEQUENCE
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DOMAIN
DOMAIN
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                               (CANP)
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Matches
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Q7SYA9
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                                                                                                                                                                     NEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M. J. Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garder A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
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01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain)
Name-CAPN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and sequence analyses of cDNA clones for the large subunits of two isozymes of rabbit calcium-dependent protease."; J. Biol. Chem. 261:9465-9471(1986).
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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MEDLINE=87279982; PubMed=3038855;
Minami Y., Emori Y., Kawasaki H., Suzuki K.;
"E-F hand structure-domain of calcium-activated neutral protease
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MEDLINE=86250902; PubMed=2424911;
Emori Y., Kawasaki H., Sugihara H., Imajoh S., Kawashima S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.9%; Score 129; DB 2; Length 713;
larity 92.9%; Pred. No. 2.1e-08;
Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Prostate;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BC061880, AAH61880.1, -. SEQUENCE 713 AA, 82119 MW; 6E664600B0EFAEBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGEDMEISVKELRTILNRIISKHKDLRT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
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Best Local Similarity
Local 26; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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CAN1 RAI P06815;

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CGANI\_RABIT TO CANI\_RABIT TO C

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Gaps

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1; Indels

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=AB; TISSUE=Whole body;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. B. Bonetow M.B., Casafer T. E.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunzarne P.H.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia B. S., Sanchez A.M.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Referention and initial analysis of more than 15,000 full-length human
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROW N.A.

STRAIN=AB; TISSUE=whole body;
Strausberg R.;
Studin=AB; TISSUE=whole body;
Strausberg R.;
Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054941; AMF494941.1,
GO; GO:0005502; C:intracellular; IEA.
GO; GO:0005502; F:calcium ion binding; IEA.
GO; GO:0005508; P:calcium ion binding; IEA.
GO; GO:0005089; P:calcium ion binding; IEA.
GO; GO:0005089; P:calcium ion binding; IEA.
INTER_PO; IPRO01090; Pept dase_C2.
Inter_PO; IPRO01090; Pept dase_C2.
Inter_PO; IPRO01090; Pept dase_C2.
FFam; PF00045; Calpain III; 1.
FFam; PF00045; EPhand; 1.
STRAI; SM00703; CysPC; 1.
SWART; SM00204; EFH: 2.
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PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00139; THTOL_PROTEASE_CYS; 1.
HYPOTHELICAL PROTEIN; EB68F95EF1A1F273 CRC64; SEQUENCE 704 AA; 80403 MW; EB68F95EF1A1F273 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Gaps

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1 AGEDMEISVKELRTILNRIISKHKDLRT 28

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Search completed: November 10, 2004, 12:27:20 Job time : 32.6358 secs

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                                                                          November 10, 2004, 11:41:17; Search time 7.74383 Seconds (without alignments) 222.664 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1 GLREESEEYMAAADEYNRLKQVKQPA 26
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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| 4656, Ap 20922, A p 20922, A p 10, App 1 12868, App 1 12868, App 1 128640, A p 22, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 10, App 1 22, App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4 App 1 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Gaps                                                                                                                                      |
| nence du nence e cue ne con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce con en ce co                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | .,                                                                                                                                        |
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| 28 45 34.4 244 4 US-09-134-000C-4656<br>29 45 34.4 257 4 US-09-248-796A-20922<br>31 45 34.4 890 3 US-09-248-796A-19207<br>31 45 34.4 1112 4 US-09-342-648-10<br>32 44.5 34.0 623 4 US-09-342-648-10<br>34 4 33.6 194 4 US-09-148-039A-128-68<br>35 44 33.6 243 3 US-08-965-037-71-718-68<br>36 44 33.6 331 4 US-09-270-767-1224<br>37 44 33.6 340 3 US-08-960-780-34<br>40 33.6 340 3 US-08-960-780-34<br>41 43.6 340 4 US-09-307-106-10<br>42 44 33.6 340 4 US-09-307-106-10<br>43 44 33.6 340 4 US-09-367-106-10<br>44 4 33.6 514 4 US-09-86-88-25-193<br>44 4 33.6 514 4 US-09-679-686B-22<br>45 44 33.6 514 4 US-09-679-686B-22<br>46 47 33.6 514 4 US-09-679-686B-22<br>47 4 4 33.6 551 4 US-09-557-006C-40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1  US-09-026-343-8  Sequence 8, Application US/09026343  Parent No. 6008018  GENERAL INTORMATION: APPLICANT: BUGNAY D. ROXANNE APPLICANT: CONAMAY GONALD C. TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELL2, A New Member of an ELL F TITLE OF INVENTION: ELSABLE FORM: MEDIUM TYPE: FIOPPY disk COMPUTER: ELSABLE FORM: MEDIUM TYPE: FIOPPY disk COMPUTER: EADABLE FORM: MEDIUM TYPE: FIOPPY disk COMPUTER: BA PC compatible COMPUTER: BAPLICATION: PRICA SPELICATION: PRICA APPLICATION NUMBER: US 60/038,447 FILING DATE: HERWATION: PRICA APPLICATION NUMBER: 19-FEB-1997 ATTORNEY/AGENT INFORMATION: MAME: GOLDSTEIN JOGNET THUMBER: 29,021 TELEPHONE: (202) 371-2600 TINFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: LOS amino acid STRANDEDNESS: not relevant MOLECULE TYPE: protein US-09-026-343-8 | Query Match 80.9%; Score 106; DB 3; Len<br>Best Local Similarity 91.7%; Pred. No. 4.6e-09;<br>Matches 22; Conservative 0; Mismatches 2; I |
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TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEO ID No: 6:
SEQUENCE CHARACTERISTICS:
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Falls Church
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                                                                                                                                                                                                                                     APPLICANT: DUAN, D. ROXANNE
APPLICANT: SHILATIFARD, ALI
APPLICANT: CONAMAY, JOAN W.
APPLICANT: CONAMAY, JOAN W.
TITLE OF INVENTION: ELLZ, A New Member of an ELL Family of
TITLE OF INVENTION: RNA POlymerase II Elongation Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.9%; Score 106; DB 3; Length 108; Best Local Similarity 91.7%; Pred. No. 4.6e-09; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08945826
Patent No. 6489460
GENERAL'INPORMATION:
APPLICANT: TSUKITA, Shoichiro
TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
COUNTRY: USA
CONFUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,871
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.0880001
TELEPHONE: (202) 372-2540
TELEPACH (202) 372-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                     3 REESEEYMAAADEYNRLKQVKQPA 26
                                                              54 REESEEYMAAADEYNRLKOVKGSA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,343
                                                                                                                                                                         Sequence 8, Application US/09362871
Patent No. 6379923
GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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STATE: D.C.
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468 REESEEYMAADEYNRLKQVKGSA 491
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US-08-945-826-2
Sequence 2, Application US/08945826;
Patent No. 6489460
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19.09-142-732-2
19.69-142-732-2
19.69quence 2, Application US/09142732
19.69quence 2, Application US/09142732
19.69quence 2, Application US/09142732
19.69quence 2, Application US/09142732
19.69quence 2, Application US/09142732
19.69quence 2, Application M. Anderson
19.60quence 3.60quence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.9%; Score 106; DB 4; Length 521; Best Local Similarity 91.7%; Pred. No. 2.9e-08; Matches 22; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE PORM:
MEDIUW TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,732
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/142,732
FILING DATE: March 14, 1997
APPLICATION NUMBER: US. 60/013,625
FILING DATE: March 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: March 15, 1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 1751-P0016B.F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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DESCRIPTION: polypeptide
FRAGMENT TYPE: complete sequence
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                               LENGTH: 521 amino acids TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-197-503-6
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3 REESEEYMAAADEYNRLKQVKQPA 26

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Sequence 2, Application US/09197503

Sequence 2, Application US/09197503

Sequence 2, Application US/09197503

Sequence 2, Application US/09197503

SENERAL NO. 655286

TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Birch, Stewart, Kolasch & Birch, LLP STREET: VA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COMPUTER: FRADABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE FORM:

MEDIUM TYPE: Abtent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

80.9%; Score 106; DB 4; Length 52
Best Local Similarity 91.7%; Pred. No. 2.9e-08;
Matches 22; Conservative 0; Mismatches 2; Indels
GENERAL INFORMATION:
APPLICANT: TSUKITA, Shoichiro
APPLICANT: TSUKITA, Shoichiro
TITLEO F INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                       COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

CONPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELA POEDY disk
COMPUTER: ELA PER FOCOMPATIBLE
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,826
FILING DATE: 05-NOV-1997
CLASSIFICATION: USA
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. JOSEPH
REFERENCE/DOCKET NUMBER: 0425-0660P
TELEPRAMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 REESEEYMAAADEYNRLKOVKGSA 491
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US-09-248-796A-20028
US-09-248-796A-20028
US-09-248-796A-20028
Sequence 20029, Application US/09248796A
Sequence 20029, Application US/09248796A
Setent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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                                                                                                                                                                Sequence 4, Application US/09197503
Patent No. 655236
GENERAL INFOMATION:
APPLICANT: TSUKITA, Shoichiro
TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
Birch, Seewart, Kolasch & Birch, LLP
SIRRET: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/945,826
FILING DATE: 05-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. Joseph
REGISTRATION NUMBER: 32,350
REFERRINGE/DOCKET NUMBER: 0425-0660P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                               467 REESEEYMAAADEYNRLKOVK 487
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  3 REESBEYMAAADEYNRLKQVK 23
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amino acid
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MOLECULE TYPE: protein
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                                                                                                                       RESULT 9
US-09-197-503-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TSUKITA, Shoichire
TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDESS:
ADDRESSES: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,826
FILING DATE: 05-NOV-1997
CLASSIFICATION: 535
                                    PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR DATE: 05-NOV-1997

ATTORNEX/AGENT INFORMATION:

NAME: FRARAI. C. JOSEPH

REGISTRATION NUMBER: 32,350

REFERENCE/DOCKET NUMBER: 0425-0660P

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 522 amino acids

TYPE: amino acid

TYPE: amino acid

MOLECULE TYPE: protein

US-09-197-503-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0425-0660P
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APPLICATION NUMBER: US/09/197,503
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NAME: FARACI, C. JOSEPH
REGISTATION UNDRER: 32,30
REFERENCE/DOCKET NUMBER: 0425-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08945826
Patent No. 6489460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 521 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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/ Fri Nov 12 14:54:55 2004
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T07.6T-00/-760-0T-8T

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Sequence 19, Application US/09849602;
Patent No. 6794501;
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Lloyd J.
TITLE REPERENCE: L0461/7105(HRV)
CURRENT APPLICATION NUMBER: US/09/849,602;
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LIENGTH: 890
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CAGANISM: Homo sapiens
US-09-849-602-19
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                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09085199B
Fatent No. 6235879
Fatent No. 6235870
GENERAL INFORMATION:
APPLICANT: Hayden, Abigail
APPLICANT: Hay, A.H.M. Mabbubul
APPLICANT: Kalchman, Anichael
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Applicate Modulators That Interact with the
TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES:
ADDRESSEE: Oppedahl & Larson
STREET: PO BOX 5270
CITY: Frisco
STATE: CO
                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.5%; Score 50.5; DB 3; Length 676; Best Local Similarity 50.0%; Pred. No. 17; Matches 11; Conservative 5; Mismatches 5; Indels
                                                                                                               Query Match 38.9%; Score 51; DB 4; Length 488; Best Local Similarity 43.5%; Pred. No. 9.5; Matches 10; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 80443-520

ZIP: 80443-520

ZIP: 80443-520

ZIP: 80443-520

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS DOS 5.0

SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B

FILING DATE:
CLASSIFICATION:
ATTORIVA AGENT INFORMATION:
NAME: LATSON, MAXINA T.
REGISTRATION NUMBER: 32038

REFERENCE POCKET NUMBER: 32038

REFERENCE POCKET NUMBER: 32038

TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 676

TUPPER AMINO ACIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
COTHER INFORMATION: Huntington-interacting protein US-09-085-1998-7
                                                                                                                                                                                                                                             117 RDATDEYF--AQEYNRFKRIFRP 137
                                                                                                                                                                                                              3 REESEEYMAAADEYNRLKOVKOP 25
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
CRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-085-199B-7
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Gaps

1;

5; Indels

Query Match
38.5%; Score 50.5; Dest Local Similarity 50.0%; Pred. No. 23;
Matches 11; Conservative 5; Mismatches

1 GLREESEEYMAAAD-EYNRLKQ 21

DB 4; Length 890;

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Sequence 4820, Application US/09134001C
; Sequence 4820, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPRENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                           RESULT 13
US-09-710-279-1660
US-09-710-279-1660
; Sequence 1660, Application US/09710279 .
; Sequence 1660, Application US/09710279 .
; Sequence 1660, Application US/09710279 .
; GENERAL INFORMATION:
; TILLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS .
; TILLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS .
; CURRENT APPLICATION NUMBER: US/09/710,279 .
; CURRENT PILING DATE: 2000-11-09 .
; PRIOR FILING DATE: 1999-11-09 .
; NUMBER OF SEQ ID NOS: 4472 .
; SOFTWARE: Patentin Ver. 2.1 .
; SEQ ID NO 1660 .
LENGTH: 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; COTHER INFORMATION: amino acid sequence US-09-710-279-1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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253 GLREEAERKASATEARYNKLKE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 SEQYFSASQQYNNLKE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SEEYMAAADEYNRLKQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-134-001C-4820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.0%; Score 48.5; DB 2; Length 83; Best Local Similarity 50.0%; Pred. No. 2.9; Matches 12; Conservative 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-U8-499-676A-10

Sequence No. 599154

Batent No. 10. Application US/08499676A

GENERAL INFORMATION:

MUMBER LOF SEQUENCES:

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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4820
LENGTH: 1211
                                                                                                                                                                                                                                             TYPE: PRT CAGANISM: Staphylococcus epidermidis US-09-134-001C-4820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 REESEEYMAAADEYN-RLKQVKOP 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|:|:||| ||:
734 SEQYFSASQQYNNLKE 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SEEYMAAADEYNRLKQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-499-676A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-499-676A-10
```

Search completed: November 10, 2004, 12:32:31 . Job time : 8.74383 secs

49 REFERRMORGOEMNGRISOIAOP 72

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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November 10, 2004, 15:53:52 ; Search time 25.0772 Seconds (without alignments) 366.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

| Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_REW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                              131
1 GLREESEEYMAAADEYNRLKQVKQPA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                               |                   |                   |                   | 0.                | 0.                | 0.                 | 4                   | ~                   |                   |                   |                   |                   | ~                    |
|-----------|-------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|---------------------|-------------------|-------------------|-------------------|-------------------|----------------------|
|           | Description                   | Sequence 19, Appl | Sequence 8, Appli | Sequence 2, Appli | Sequence 104, Apr | Sequence 900, App | Sequence 1982, Ap  | Sequence 18880, P   | Sequence 19971, 2   | Sequence 6, Appli | Sequence 6, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 51864, A    |
| SUMMARIES | DB ID                         | US-10-092-750-19  | US-10-028-780-8   | US-09-891-064A-2  | US-10-176-847-104 | US-10-601-953-900 | US-10-094-749-1982 | US-10-369-493-18880 | US-10-369-493-19971 | US-09-748-875-6   | US-09-298-523B-6  | US-09-748-875-4   | US-09-298-523B-4  | US-10-282-122A-51864 |
|           | 90                            | 14                | 13                | σ                 | 14                | 15                | 14                 | 14                  | 14                  | σ                 | 10                | σ                 | 0                 | 15                   |
|           | %<br>Query<br>Match Length DB | 26                | 108               | 522               | 522               | 522               | 175                | 330                 | 330                 | 481               | 481               | 496               | 496               | 1163                 |
|           | %<br>Query<br>Match           | 100.0             | 80.9              | 6.08              | 80.9              | 80.9              | 42.0               | 40.5                | 39.7                | 39.7              | 39.7              | 39.7              | 39.7              | 39.7                 |
|           | Score                         | 131               | 106               | 106               | 106               | 106               | 55                 | 53                  | 52                  | 52                | 52                | 52                | 52                | 52                   |
|           | Result<br>No.                 | Н                 | 0                 | m                 | 4                 | S                 | 9                  | 7                   | œ                   | σ                 | 10                | 11                | 12                | 13                   |

| 404                                      | Seguence 286036,<br>Seguence 70920, A<br>Seguence 199277, | 7 (7                               | 10810,                | 4.0              | 4                | 58323,           | O O                                | 53048,          | 59957,          | 286034           | 286035          | 286038           | 37032,          | 39618,          | Ō               | equence 63528   | 8696           | equence 15863  | equence 3357   | 7611           | 16, 1         | 19<br>26     | e 16, 1      |
|------------------------------------------|-----------------------------------------------------------|------------------------------------|-----------------------|------------------|------------------|------------------|------------------------------------|-----------------|-----------------|------------------|-----------------|------------------|-----------------|-----------------|-----------------|-----------------|----------------|----------------|----------------|----------------|---------------|--------------|--------------|
| 369-493-13544<br>382-227-8<br>349-602-19 | .0-425-115-<br>10-282-122A<br>10-425-115-                 | 10-767-701-5486<br>10-425-114-7025 | 10-739-930-1081       | 10-425-114-45740 | 10-425-114-47386 | 10-425-114-58323 | 10-425-115-2408<br>10-425-115-2860 | 10-425-114-5304 | 10-425-114-5995 | 10-425-115-28603 | 10-425-115-2860 | 10-425-115-28603 | 10-425-114-3703 | 10-425-114-3961 | 10-425-114-6036 | 10-425-114-6352 | -10-156-761-96 | -10-437-963-15 | -10-320-797-33 | -10-032-585-76 | -10-262-313-1 | 10-768-878-1 | -09-992-331- |
| 10<br>10<br>10                           | 15<br>15                                                  | 16                                 | 17                    | 12               | 15               | 15               | 17                                 | 12              | 15              | 17               | 11              | 17               | 15              | 15              | 15              | 15              | 14             | 16             | 12             | 14             | 14            | 16           | 10           |
| 1126<br>110<br>890                       | 305<br>1189                                               | 152                                | 617                   | 634              | 255              | 285              | 0 0<br>0 0<br>0 0                  | 300             | 300             | 307              | 307             | 307              | 308             | 308             | 308             | 308             | 311            | 359            | 1465           | 1948           | 426           | 426          | 428          |
| 88.8<br>9.8.0<br>9.10.0                  |                                                           |                                    |                       |                  | ٠,               | 7.               | ~ ~                                |                 | ~               | ~                | 7.              | ۲.               | ~               | 7               | 7.              | -               | 7              | 7              | 7              | 7              | 7             | 37.0         | 7            |
| 50.5<br>50.5<br>50.5                     | ν<br>0 0 0<br>0 0                                         | 9.6                                | 24.04<br>0.04<br>0.04 | · o              | 4, 4,<br>V Q     | 49               | 4<br>9<br>9                        | 49              | 49              | 49               | 4.0             | 49               | 49              | 49              | 49              | 49              | 49             | 49             | 49             | 4.0            | ω.            | 48.5         | æ            |
| 14<br>15<br>16                           | 17                                                        | 10.0                               | 22.                   | 100              | 9 n              | 27               | 2 7 7 8                            | 30              | 31              | 32               | 33              | 34               | 35              | 36              | 3.7             | 38              | 39             | 40             | 41             | 42             | 43            | 44           | 45           |

### ALIGNMENTS

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Gaps
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RESULT 1
US-10-092-750-19
is Sequence 19, Application US/10092750
j Publication No. US2003003157A1
j GENERAL INFORMATION:
j APPLICANT: Hammond, Philip W.
j APPLICANT: Hammond, Philip W.
j TITLE OF INVENTION: POLYPEPTIGES Interactive with BCL-X1
TITLE OF INVENTION: POLYPEPTIGES:
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US 60/274,526
pRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SEQ ID NO 19
IENGTH: 26
IENGTH: 26
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1 GLREESEEYMAAADEYNRLKQVKQPA 26 RESULT 2
US-10-028-780-8
Sequence 8, Application US/10028780
Publication No. US20020132329A1
GENERAL INFORMATION:

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Sequence 2, Application US/09891064A

Petent No. US20020082391A1

GENERAL INPORMATION:
APPLICANT: James M. Anderson
APPLICANT: Christina M. Van Itallie
TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
TITLE OF INVENTION: Absorption Using Occludin Inhibitors
FILE REFERENCE: OCR-754 CIP
CURRENT FALING DATE: 1098-09-15
PRIOR PLING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 2
IEBNGTH: 522
TYPE: PRIT
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Gaps

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-176-847-104
    ORGANISM: Homo sapiens
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US-10-601-953-900
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APPLICANT: DUAN, D. ROXANNE
SHILATIFARD, ALI
CONAMAY, JOAN W.
CONAMAY, RONALD C.
TITLE OF INVENTION: ELLZ, A New Member of an ELL Family of
RNA POlymerase II Elongation Factors
                                                                                                                           NUMBER OF SEQUENCES: 334
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

80.9%; Score 106; DB 13; Length 108;
Best Local Similarity 91.7%; Pred. No. 3.5e-07;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                    STATE: D.C.
CONTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/028,780
FILING DATE: 28-Dec-2001
CLASSIFICATION NUMBER: US/09/026,343
FILING APPLICATION NUMBER: US/09/026,343
FILING DATE: CURROWN-
APPLICATION NUMBER: US 60/038,447
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INPORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.0880001
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: No. US20020132329Al Relevant
; TOPOLOGY: No. US20020132329Al Relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-028-780-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 REESEEYMAAADEYNRLKQVKQPA 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-891-064A-2
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APPLICANT: Outy, Steven C.

TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Unctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therepeutic Compounds
FILE REFERENCE: 02-03US
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTMARE: Patentin version 3.2
SOFTMARE: Patentin version 3.2
LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4

US-10-176-847-104

US-10-176-847-104

Sequence 104, Application US/10176847

Publication No. US200300686361

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: AND COVALAN CANCER

TITLE OF INVENTION: AND COVALAN CANCER

TITLE OF INVENTION: MRI-039

CURRENT APPLICATION NUMBER: US/10/176,847

CURRENT FILING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 112

SOOTHWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106; DB 14; Length 522;
Pred. No. 2e-06;
0; Mismatches 2; Indels
                                                                                                                                                               Query Match 80.9%; Score 106; DB 9; Length 522; Best Local Similarity 91.7%; Pred. No. 2e-06; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-900
                                                                                                                                                                                                                                                                                                                                     468 REESEEYMAAADEYNRIKOVKGSA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 REESEEYMAAADEYNRLKOVKGSA 491
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Publication No. US20040077540A1
GENERAL INFORMATION:
FEATURE:
NAWE/KEY: peptide
LOCATION: complete sequence
CTER INFORMATION: human occludin
US-09-891-064A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative C
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US-10-369-493-19971

) Sequence 19971, Application US/10369493

) Sequence 19971, Application US/10369493

) Publication No. US20030233675A1

) Publication No. US20030233675A1

) APPLICANT: Cao, Yongwei

APPLICANT: Einkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

) TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

PILE REFERENCE: 38-10(5202)B

) TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

PILE REFERENCE: 38-10(5202)B

) PRIOR APPLICATION UNMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

) WUMBER OF SEQ ID NOS: 47374

) SEQ ID NO 19971

LENGTH: 330
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Sequence 6, Application US/09748875

Publication No. US20010016200A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REPERENCE: 454312-3140.
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 6

LENGTH: 481
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                                                                                               Query Match 40.5%; Score 53; DB 14; Length 330; Best Local Similarity 45.5%; Pred. No. 33; Matches 10; Conservative 7; Mismatches 5; Indels
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39.7%; Score 52; DB 9; Length 481;
Best Local Similarity 39.1%; Pred. No. 69;
Matches 9; Conservative 6; Mismatches 8; Indels
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39.7%; Score 52; DB 14;
Best Local Similarity 45.5%; Pred. No. 46;
Matches 10; Conservative 7; Mismatches 5.
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                                                                                                                                                                                                 2 LREESEEYMAAADEYNRIKOVK 23
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12 LRQEGEKAIAAADTLERLEELR 33
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ORGANISM: Streptococcus pneumoniae
                       ; ORGANISM: Anabaena PCC7120
US-10-369-493-18880
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Sequence 18880, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION: USCONSO233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Gldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B1

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 18880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SCHIKAWA, TSUTOMU
APPLICANT: OTSUKA, NOTSUKA, TSUTOMU
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASUGO, YASUHIKO
TILE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: uS/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALENT VET. 2.1
SOFTWARE: PALENT VET. 2.1
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Best Local Similarity 52.4%; Pred. No. 6
Matches 11; Conservative 2; Mismatch
                                             468 REESEEYMAAADEYNRLKQVKGSA 491
3 REESEEYMAAADEYNRLKOVKOPA 26
                                                                                                                                                                       Sequence 1982, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                         APPLICANT: SUGGAI, TAKAO
APPLICANT: SUGGIYAMA, TCMOVASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: HIO, YUKI
APPLICANT: HIO, YUKI
APPLICANT: NAGAI, KENICHI
APPLICANT: NAGAI, KENICHI
APPLICANT: NAGAI, KENICHI
APPLICANT: NAGAI, KENICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-1982
                                                                                                                       RESULT 6
US-10-094-749-1982
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: BLITTA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                          Query Match 39.7%; Score 52; DB 10; Length 496; Best Local Similarity 39.1%; Pred. No. 72; Matches 9; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 51864, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                    461 QQAEEDYARRSEEYNRLTQQQPP 483
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                                                                      , ORGANISM: Streptococcus pneumoniae US-09-298-523B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 EASKEYLKAEEEYNEGKEV 248
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tarwick, John
APPLICANT: Tarwick, John
APPLICANT: Farsylh, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.7%;
ilarity 52.6%;
Conservative 4
PatentIn Ver.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                               RESULT 13
US-10-282-122A-51864
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SOFTWARE: Pat
SEQ ID NO 4
LENGTH: 496
TYPE: PRT
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                                                                                Squence 6, Application US/09298523B
Publication No. US20030059438A1
GENERAL INVORMATION:
APPLICANT: BRILES et al.
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS;
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/298,523B
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTI Ver. 2.1
SSQ ID NO 6
LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09298523B
Publication No. USZ0030059438A1
Publication No. USZ0030059438A1
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/298,523B
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09748875
Publication No. US20010016200A1
GENERAL INFORMATION:
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REPERENCE: 444312-3146
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
RIGHER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4.
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69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB
Pred. No. 69;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52;
Pred. No.
446 QQAEEDYARSEEEYNRLTQQQPP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 QQAEEDYARSEEEYNRLTQQQPP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: |:| ::| :: | ... | | | ... | | ... | 461 QQQPP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 REESEEYMAAADEYNRLKOVKOP 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 REESEEYMAAADEYNRLKQVKQP 25
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-298-5238-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 39.1%;
Matches 9; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.1%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-298-523B-4
                                                         RESULT 10
US-09-298-523B-6
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US-09-748-875-4
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0
Score 52; DB 15; Length 1163;
Pred. No. 1.8e+02;
4; Mismatches 5; Indels 0
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Sequence 13544, Application US/10369493
Sequence 13544, Application US/203023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Glame, Barry S.
APPLICANT: Glame, Barry S.
APPLICANT: Glame, Barry S.
APPLICANT: Glame, Warry S.
APPLICANT: Glame, Warry S.
APPLICANT: Glame, Warry S.
APPLICANT: Glame, Walleng S.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION WUMBER: US/10/369, 493
CURRENT FILING DATE: 2002-22
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13544
LENTE 1126
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Best Local Similarity 37.5%; Pred. No. 23;
Matches 9; Conservative 9; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                              38.9%; Score 51; DB 14; Length 1126; 69.2%; Pred. No. 2.4e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 10, 2004, 16:36:03 Job time: 26.0772 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:::|| :::|
81 LKQRNSEYKGESDKYKNRIKELEQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LREESEEYMAAADEY-NRLKQVKQ 24
                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Thermoplasma volcanium US-10-369-493-13544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 EEFIAAEDEYNKL 364
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 10, 2004, 11:36:51 ; Search time 5.25617 Seconds (without alignments) 475.942 Million cell updates/sec

US-10-092-750-19 131 1 GLREESEEYMAAADEYNRLKQVKQPA 26

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| . 4       | pt            | occludin - human | •      | ica    | prot   | - trna | spliceosome-associ | ATPase involved in | hypothetical prote | hypothetical prote | hypothetical profe |        |        | Ņ      | pti    |        | - 12   | capsid | outer capsid spike | luxQ protein - Vib | protein F21J9.12 [ | σ      | Slyl protein - rat | hypothetical prote | •-    |        | Sugar-binding peri | vlne-like (mynonla | hypothetical prote | ıн  |
|-----------|---------------|------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-------|--------|--------------------|--------------------|--------------------|-----|
| SUMMARIES | ΙD            | G02533           | A49467 | T05409 | A71921 | AE2411 | A55749             | G97236             | H75200             | D71234             | S77001             | E64591 | T24492 | S30508 | C97142 | D85045 | VPXRPC | S45061 | 845060             | S49046             | F86378             | S59373 | JC4674             | T23537             | LWLV1 | D69487 | A96982             | 9060               | T21588             | 248 |
|           | DB            |                  | 7      | ~      | ~      | ~      | ~                  | N                  | ~                  | N                  | 7                  | N      | ~      | C)     | ~      | ~      | Н      | ~      | ~                  | N                  | ~                  | N      | N                  | N                  | -     | Ŋ      | 7                  | 7                  | ~                  | 7   |
|           | Length        | 522              | 504    | 764    | 110    | 330    | 501                | 1163               | 300                | 300                | 339                | 110    | 406    | 428    | 158    | 228    | 736    | 744    | 744                | 853                | 1864               | 323    | 648                | 878                | 184   | 221    | 378                | 682                | 2025               | 9   |
| , e)e     | Query         |                  | 45.0   | ٠      |        | 40.5   | 40.5               | φ.                 | 39.3               | σ.                 | æ                  | æ      | 37.4   | ۲.     | ė.     | ů.     | Ġ      | 'n     | 36.6               | 'n                 |                    | 'n     | 'n                 | 'n                 | 'n    | 35.1   | 35.1               | 35.1               | 35.1               | 10  |
|           | Score         | 106              | n<br>O | S      | 53.5   | 53     | 53                 | S                  | •                  | i                  | 51                 | 50.5   | 49     | 48.5   | 48     | 4.8    | 48     | 48     | 48                 |                    | 84                 | 47     | 47                 | 47                 | 46    | 46     | 46                 |                    | 46                 |     |
|           | Result<br>No. | н                | 7      | m      | 4      | S      | ø                  | 7                  | ω                  | σ                  | 10                 | 11     | 12     | 13     | 14     | 15     | 16     | 17     | 18                 | 19                 | 50                 | 21     | 22                 | 23                 | 24    | 25     | 56                 | 27                 | 28                 | 0   |

| hypothetical prote | L-arabinose isomer | probable acetyltra | hypothetical prote | hypothetical prote | hypothetical prote | TPR-repeat-contain | conserved hypothet | hypothetical prote | probable cell divi | probable protein k | hypothetical prote | long-chain-fattv-a | proline dehydrogen | malate dehydrogena | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T34418             | B72398             | B83143             | AD1978             | T43194             | T45994             | C97031             | A86837             | T39310             | H71331             | T41623             | T43152             | 523052             | C81297             | A53318             | B90975             |
| N                  | 0                  | ~                  | N                  | ď                  | 7                  | ~                  | ~                  | 7                  | N                  | 7                  | ~                  | ~                  | N                  | N                  | (7)                |
| 3488               | 496                | 153                | 167                | 321                | 325                | 359                | 366                | 401                | 418                | 206                | 515                | 200                | 1162               | 601                | 732                |
|                    |                    | 4                  | 4                  | 4.                 | 4.                 | 4.                 | 4.                 | 4.                 | 4.                 | 4.                 | 4.                 | 34.4               | 34.4               | 0.                 | 0.                 |
| 35.1               | 34.7               | 34.                | 34.                | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | ň                  | 34                 |
| 46 35.1            | 45.5 34.7          | 45 34.             | 45 34.             | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 45 34              | 44.5 34            | 44.5 34            |

## ALIGNMENTS

Occludin - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: G0253
R.Van Itallie, C.M.
A.Reference number: H01403
A.Accession: G02533
A.Accession: G02533
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Rocessions: G02533
A.Molecule type: mRNA
A.Residues: 1522 vVAN>
A.Coss-references: UNIPROT:Q16625; EMBL:U53823; NID:g1322281; PIDN:AAB00195.1; PID:g132; C; Superfamily: occludin

Length 522; Query Match 80.9%; Score 106; DB 2; Length 52 Best Local Similarity 91.7%; Pred. No. 8.3e-07; Matches 22; Conservative 0; Mismatches 2; Indels

Gaps ö

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RESULT 2
A49467
occludin - chicken
CiSpecies: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004
C;Accession: A49467
R;Furuse, M.; Hirase, T.; Itoh, M.; Nagafuchi, A.; Yonemura, S.; Tsukita, S.; Tsukita, S.
J.;Cell Biol. 123, 1777-1788, 1993
A;Title: Occludin: a novel integral membrane protein localizing at tight junctions.
A;Reference number: A49467
A;Reference number: A49467
A;Status: preliminary
A;Molecule type: many
A;Residues: L-504 <FUR>
A;Residues: 1-504 <FUR>
A;Cross-references: UNIPROT:Q91049; GB:D21837; NID:g464148; PIDN:BAA04865.1; PID:g540494
C;Superfamily: occludin
C;Reywords: liver; membrane protein\_

ö Query Match
Best Local Similarity 43.5%; Pred. No. 2.3;
Matches 10; Conservative 7; Mismatches 6; Indels

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Gaps

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A;Cross-references: UNIPROT:Q8YMT4; GB:BA000019; PIDN:BAB76544.i; PID:g17133982; GSPDB:GR A;Experimental source: strain PCC 7120
Genetical Source: strain PCC 7120
A;Genetical Strain Strain PCC 7120
C;Superfamily: phenylalanine-tRNA ligase alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-501 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
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ABES411

phenylalanyl-tRNA synthetase alpha chain [imported] - Nostoc sp. (strain PCC 7120)

C./Species: Nostoc sp. PCC 7120

C./Species: Nostoc sp. PCC 7120

C./Actesion: AE2411

R./Note: 14-Dec-2011 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C./Actession: AE2411

R./Saneko, T.; Nakanura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

A./Title: Complete Genomic Sequence of the Filamentous Nirrogen-fixing Cyanobacterium Ana A./Accession: AE2411

A./Accession: AE2411

A./Accession: AE2411

A./Accession: AE2411

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A./Acces
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()Species: Helicobacter pylori

A, Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.;

I Ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A1800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 «ARN»
A;Cross-references: UNIPROT:Q9ZLQB; GB:AE001485; GB:AE001439; NID:g4155057; PIDN:AAD061C
A;Experimental source: strain J99
                                                                                                         hypothetical protein F10M6.170 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Ozecies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05409 R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; submitted to the Protein Sequence Database, February 1938 A;Reference number: 215414 A;Reference number: 215414
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40.8%; Score 53.5; DB 2; Length 110;
Best Local Similarity 41.7%; Pred. No. 2.6;
Matches 10; Conservative 8; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.0%; Score 55; DB 2; Length 764; 45.0%; Pred. No. 13; ive 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: DNA
A Residues: 1-764 - EBEV>
A) Fresidues: 1-764 - EBEV>
A) Cross-references: UNITROT:049371; EMBL:AL021811
A; Experimental source: cultivar Columbia; BAC clone £10M6
C; Genetics:
A; Map Dosition: 4
A;Note: F10M6.170
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Matches 9; Conservative
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Spliceosome-associated protein SAP 61 - human
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Date: 23-Mar.1995 #sequence revision 23-Mar.1995 #text_change 09-Jul-2004
C,Accession: A55749; S53883; S49319
R;Chiara, M.D.; Champion-Arnaud, P.; Buvoli, M.; Nadal-Ginard, B.; Reed, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 6403-6407, 1994
A.Title: Specific protein-protein interactions between the essential mammalian spliceoson
A,Reference number: A55749; MUID:94294390; PMID:8022796
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A;Cross-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:G}
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPROT:Q12874; GB:U08815; NID:g508722; PIDN:AAA19625.1; PID:g508723 R, Kraemer, A.; Legrain, P.; Milhauser, F.; Groening, K.; Brosi, R.; Bilbe, G. R. Mulcleic Acids Res. 22, S233-S238, 1994 A; Mulcleic Acids Res. 22, S233-S238, 1994 A; Title: Splicing factor SF3a60 is the mammalian homologue of PRP9 of S. cerevisiae: the A; Reference number: S53583; MUID:95116308; PMID:7816610
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A,Status: preliminary; nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-175, G',177-501 <KRA>
A,Cross-references: EMBL:X81789; NID:G551449; PIDN:CAA57388.1; PID:G551450
                                                                                                      Gaps
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Query Match 40.5%; Score 53; DB 2; Length 330; Best Local Similarity 45.5%; Pred. No. 9.8; Matches 10; Conservative 7; Mismatches 5; Indels
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40.5%; Score 53; DB 2; Length 501;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 12; Conservative 6; Mismatches 6; Indels
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loffuls, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.h. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T24492
R;Sulston, J
submitted to the EMBL Data Library, November 1995
A;Reference number: Z18898
A;Accession: T24492
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reference number: UNIPROT:Q22192; EMBL:Z68108; PIDN:CAA92135.1; GSPDB:GN00028; CESP:T0:
A;Ross-references: UNIPROT:Q22192; EMBL:Z68108; PIDN:CAA92135.1; GSPDB:GN00028; CESP:T0:
C;Genetics:
A;Reperimental source: clone T05Al0
C;Genetics:
A;Rap Position: X
A;Nap Position: X
A;Ittrons: S0/1; 76/3; 98/3; 131/1; 167/3; 242/1; 294/1; 384/3
                                                                                                                                                                A,Accession: S77001
A,Status; mucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Rosidues: 1-339 <KAN>
A,Cross-references: UNIPROT:055928; EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA1069:
A,Cross-references: UNIPROT:055928; EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA1069:
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Superfamily: mutr domain homology <MUTI>
F;228-262/Domain: mutr domain homology <MUTI>
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     A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Residues: 1-110 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein HP0573 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug.1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64591
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                                                                                                                  A;Reference number: S74322; MUID:97061201; PMID:8905231
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38.5%; Score 50.5; DE
Best Local Similarity 37.5%; Pred. No. 6.7;
Matches 9; Conservative 9; Mismatches
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38.9%; Score 51; DB
Best Local Similarity 47.6%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches
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81 LKQRNSEYKGESDKYKNRIKELEQ 104
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Cispecias: V: Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir

R; Rawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A; Feterence number: A71000, MUID:98344137; PMID:9679194

A; Reterence number: A71000, MUID:98344137; PMID:9679194

A; Reterence number: A71000, MUID:98344137; PMID:9679194

A; Reterence number: A7100, MUID:98344137; PMID:9679194

A; Reterence number: A7100, MUID:98344137; PMID:9679194

A; Residues: 1-300 «KAW»

A; Residues: 1-300 «KAW»

A; Residues: 1-300 «KAW»

A; Residues: 1-300 «KAW»

A; Residues: 1-300 «KAW»

A; Recentinental source: strain OT3

A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PAB0081 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R;Anonymous, Genoscope
Submitted to the EMBi Data Library, July 1999
A;Beference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference preliminary
A;Residue: preliminary
A;Residues: 1-300 «KAW»
A;Residues: U300 «KAW»
A;Residues: U300 «KAW»
A;Residues: U300 «KAW»
A;Residues: U300 «KAW»
A;Residues: U300 «KAW»
A;Residues: U300 «KAW»
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Synochetical protein slr0787 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

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C;Species: Synechocystis sp.

C;Avariety: PCC 6803

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Score 48; DB 2; Pred. No. 32; 8; Mismatches

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A, Status: preliminary
A, Status: DNA
A, Molecule type: DNA
A, Residues: 1-228 <STO>
A, Cross-references: UNIPROT: Q9SY36; GB: NC_001268; NID: g7270681; PIDN: CAB77843.1; GSPDB: GP.
C, Genetics:
A, Genetics: A14gol380
A, Map position: 4
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Best Local Similarity 34.8%;
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A; Accession: D85045
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R;Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A;Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression A;Reference number: S30508; MUID:93066220; PMID:1279674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428 <MBY.>
A;Cossireferences: UNIPROT:P30936; EMBL:X63574; NID:956315; PIDN:CAA45130.1; PID:956316
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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(Cross-references: UNIPROT: 097HP4; GB: AE001437; PIDN: AAK79926.1; PID: 915024946; GSPDB:G
Experimental source: Clostridium acetobutylicum ATCC824
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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C.Superfamily: transcription elongation factor greb
C.Keywords: transcription factor
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Pred. No. 22;
4; Mismatches
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Pred. No. 54;
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                                                                                   ||::|: :||: ||321 REQEDEHKRRMEEYHRREQERQEA 344
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           26
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                 3 REESEEYMAAADEYNRLKQVKQPA
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Best Local Similarity 50.0%;
Matches 12; Conservative 1
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Best Local Similarity 42.9%;
Matches 12; Conservative
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Molecule type: DNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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Run on:

November 10, 2004, 11:27:01; Search time 28.4475 Seconds (without alignments) 525.871 Million cell updates/sec

US-10-092-750-19

131 1 GLREESEEYMAAADEYNRLKQVKQPA 26 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description         | 097766 sus scrofa | O6pp84 bos taurus | Aat00455 bos tauru | Q61146 mus musculu | Bac31298 mus muscu | Q16625 homo sapien | ij     | Q9z303 rattus norv | ratt     | nis        | canis fa | Q9punl xenopus lae | Q6nrr0 xenopus lae |          | Q91049 gallus gall | Q28793 potorous tr |        | Aah67178 brachydan | Q96aal homo sapien |        |          | Q61112 mus musculu | Q91zs3 rattus norv | шnв      | Q9brk5 homo sapien | 7zue7  |      | arabidopsi | arabidopsi | licop  | Q6tuf1 rattus norv |
|-----------|---------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|----------|------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------|--------------------|--------------------|--------|----------|--------------------|--------------------|----------|--------------------|--------|------|------------|------------|--------|--------------------|
| SUMMARIES | ID                  | 097766            | O6PP84            | AAT00455           | OCEN MOUSE         | BAC31298           | OCLN HUMAN         | QGPGTS | Q9Z303             | AAH62037 | OCLN CANFA | C9NOW3   | OCLN_XENLA         | Q6NRR0             | AAH70670 | OCEN CHICK         | OCLN_POTTR         | 66XN9Q | AAH67178           | Q96AA1             | Q7ZUC2 | AAH66581 | CB45_MOUSE         | CB45_RAT           | AAH68152 | CB45 HUMAN         | Q7ZUE7 |      | Q8H1E5     | Q9C5L5     | O9ZLQ8 | Q6TUF1             |
|           | DB                  |                   | N                 | ~                  | Н                  | 7                  | -                  | N      | N                  | N        |            | N        | Н                  | N                  | N        | Н                  | Н                  | N      | N                  | ~                  | 0      | 0        | H                  | Н                  | N        | H                  | N      | N    | N          | 7          | ~      | (1)                |
|           | Length              | 121               | 449               | 449                | 521                | 521                | 522                | 523    | 523                | 523      | 521        | 260      | 493                | 497                | 497      | 504                | 489                | 500    | 500                | 259                | 356    | 356      | 361                | 361                | 361      | 362                | 492    | 764  | 783        | 783        | 110    | 230                |
|           | %<br>Query<br>Match |                   | 80.9              | 80.9               | 80.9               | 80.9               | 80.9               | 80.9   | 80.9               | 80.9     | 80.2       | 80.2     | 60.3               | 48.9               | 48.9     | 45.0               | 44.3               | 42.7   | 42.7               | 42.0               | 42.0   | 42.0     | 42.0               | 42.0               | 42.0     | 42.0               | 42.0   | 42.0 | N          | 42.0       | 40.8   | 40.5               |
|           | Score               | 10                | 106               | 0                  | 0                  | 0                  | 0                  | 0      | 0                  | 0        | 0          | 0        | 79                 | 64                 | 64       | 59                 | 58                 | 56     | 26                 | 55                 | 55     | 55       | 55                 | 55                 | 55       | 55                 | 55     | ຄ    | ស          | വ          | 53.5   | 53                 |
|           | Result<br>No.       |                   | 8                 | ო                  | 4                  | Ω                  | ø                  | 7      | ω                  | თ        | 10         | 11       | 12                 | 13                 | 14       | 15                 | 16                 | 17     | 18                 | 19                 | 20     | 21       | 22                 | 23                 | 24       | 25                 | 26     | 27   | 28         | 29         | 30     | 31                 |

| Aag91049 rattus no<br>ORvmt4 anabaena sp | Q12874 homo sapien | Q9d554 mus musculu | Bac27111 mus muscu | Q7vg33 helicobacte | Q8ggw4 acinetobact | Q97fk1 clostridium | O57874 pyrococcus | Q9v2e3 pyrococcus | Q948f7 oryza sativ | Q8u412 pyrococcus | Q6dhe7 brachydanio | Q55928 s bifunctio |
|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|
| AAQ91049<br>SVF2 ANASP                   | S3A3_HUMAN         | S3A3 MOUSE         | BAC27111           | Q7VG33             | Q8GQW4             | SBCC CLOAB         | 057874            | Q9V2E3            | Q948F7             | Q8U4L2            | Q6DHE7             | NADM_SYNY3         |
| 0 -                                      | ı ,-ı              | Н                  | 7                  | N                  | N                  | ٦                  | N                 | ~                 | N                  | 0                 | ~                  | н                  |
| 230                                      | 501                | 501                | 501                | 827                | 988                | 1163               | 300               | 300               | 219                | 300               | 325                | 339                |
| 40.5                                     | 40.5               | 40.5               | 40.5               | 39.7               | 39.7               | 39.7               | 39.3              | 39.3              | 38.9               | 38.9              | 38.9               | 38.9               |
| 53                                       | 5 2                | 53                 | 23                 | 52                 | 52                 | 25                 | 51.5              | 51.5              | 51                 | 51                | 51                 | 51                 |
| 32                                       | . 8<br>4           | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                | 42                 | 43                | 44                 | 45                 |

# ALIGNMENTS

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[1] --SEQUENCE FROW N.A. TISSUE-Retinal endothelium; Sundstrom J.M., Felinski E.A., Phillips B., Antonetti D.A.;

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man, mouse, dog, and rat-kangaroo homologues."; Cell Biol. 133:43-47(1996).
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A., Itoh M., Yonemura S., Furuse M., Tsukita S., "Interspecies diversity of the occludin sequence: cDNA cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Retinal endothelium;
Sundstrom J.M., Felinski E.A., Phillips B., Antonetti D.A.;
"Bos taurus occludin gene.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYE09500;
AAT00455.1;
NON_TER
                                                                                                                                                                                                                                          80.9%; Score 106; DB 2; Length 449; 91.7%; Pred. No. 3.1e-06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.9%; Score 106; DB 2; Length 449; 91.7%; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
SEQUENCE 449 AA; 50627 MW; 235BE8259CF05D1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT00455;
10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Occludin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 AA.
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                                                                                                                                                                                                                                                                                                                                                                 395 REESEEYMAAADEYNRLKQVKGSA 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 REESEEYMAAADEYNRLKOVKOPA 26
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TISSUE-Lung;
MEDLINE-96181088; PubMed-8601611;
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7*
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nes 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Ocln; Synonyms=Ocl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
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Q61146;
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REQUENCE FROM N.A.

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RESULING—25354683; PubMed=21466851, DOI=10.1038/nature01266;

RA MISAIN—C57BL/6J; TISSUB—COVATY, and Uterus;

RA Misaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Misaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Madaid. I., M., Kanapin A., Matsuda H., Batalov S., Beisel K.M.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Clackenbush J.,

RA Baldarelli R., Fractor V., Chothia C., Corbanch L. S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., King B.L.,

RA Manalotto D.S., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertae G., Pesole G.,

RA Ravasi T., Reed D.G., Reed D.U., Reid J., Rings B.Z., Ringwald M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultena R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Vana Z., Zavolan M., Zhu Y., Zimmer A., Kandan M., Sato K.,

RA Shiraki T., Wash K., Kawai J., Aiamawa T., Pukuda S.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagwa I.,

RA Minakaki A., Sakai K., Sasaki D., Shibata R., Shinagawa I.,

RA Minakaki A., Sakai K., Sasaki D., Shibata R., Shinagawa I.,

RA Hara A., Hashizaki Y.,

RA Hirozane-Kishikawa T., Ronno R., Lander E.S., Rogers J.,

RA Hirozane-Kishikawa T.,

RA Hara A., Hashizaki Y.,

RA Hirozane-Kishikawa T.,

RA Shiraki T.,

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DevELOOPMENTAL STAGE: Found diffusely on the lateral membranes of Sertoli calls in the early prepubertal period. With development, became gradually concentrated at the most basal regions of Sertoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Necessary for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction (By similarity).
-!- PTM: Phosphorylated (By similarity).
-!- SIMILARITY: Belongs to the ELL / occludin family.
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MEDLINE=20530913; PubMed=11076861;
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STRAIN-657BL/64; TISSUB=Cerebellum;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                             Gaps
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14-APR-2004 (TrEMBLrel. 27, Last annotation update)
1 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007C19 product:occludin, full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                      Tight junction; Transmembrane. Cytoplasmic (Potential).
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Extracellular (Potential)
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21D62F370EB33E7D CRC64;
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Cytoplasmic (Potential).
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STRAIN=CS7BL/60; IISSUB=Cerebellum;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol, 303:19-44(1999).
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STRAIN-CS7BL/6J; TISSUE-Cerebellum;
MEDLINE-21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
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STRAIN-CSTBALL 64; TISSUE-Cerebellum;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
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                        Phosphorylation;
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STRAIN-CSBL/67 TISSUE-Cerebellum;
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A ratuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hirancto K., Hiracka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Konno H., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A gawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
A Comaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
B SEQUENCE 521 AA, 58999 MW; 21D62F370BB33E7D CRC64;
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Rawai J., Raw
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BISILINE=26181088 PubMed=8601611;

Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
Itoh M., Yonemura S., Furuse M., Tsukita S.;

"Interspecies diversity of the occludin sequence: cDNA cloning of human, mouse, dog, and ra--kangaroo homologues.";

J. Cell Biol. 133:43-47(1996).
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van Itallie C.M., Fanning A.S., Anderson J.M.;
Submitted (MAY-1996) to the EMBL/GenBark/DDBJ databases.
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"Genomic structure of occludin gene.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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TISSUE=Brain, and Lung;
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                             Attausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Attausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A hopkins R.F., Jordan H., Mooze T., Max S.I., Wang J., Hsieh F.,
A batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A baltchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A branchein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.J., Mallek J.A., Glubs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley W.C., Sochento Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. M., Krzywinski M.I., Skalaka J., Smallus D.E.,
Butterfield X.S. N., Krzywinski M.I., Skalaka J., Smallus D.E.,
Butterfield X., S.N., Krzywinski M.I., Skalaka J., Smallus D.E.,
Brands D.N., March D.N., Marra M.A.,
Brands D.N., March M.A., Marra M.A.,
Brands D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., March M.A.,
Brands D.N., March D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., March D.N., Marra M.A.,
Brands D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N., March D.N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."

Throc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

I Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

I Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

I SUBCITION: U.S.A. 100-1101 (2000).

I SUBCELLULAR LOCATION: Integral membrane protein.

I SUBCELLULAR LOCATION: Integral membrane protein.

I SUBCELLULAR LOCATION: Integral membrane protein.

I SUBCELLULAR LOCATION: Integral membrane protein.

I SUBCELLULAR LOCATION: Integral membrane protein.

I SUBCELLULAR LOCATION: Integral of the tight junction of the tight junction of the tight junction of the tight junction of the tight junction of the tight junction (By similarity).

I SUMILARITY: Belongs to the ELL / occludin family.
   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tight junction; Transmembrane. Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
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Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM, 602876; -.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0006461; P:protein complex assembly; TAS.
InterPro; IPR002853; Marvel.
InterPro; IPR002958; Occludin.
InterPro; IPR010844; Occludin.
Pfam; PF01284; MAVEL, 1.
PRINTS; PR01258; OCCLUDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEL; AF400630; AAL47094'1; EMEL; AF400633; AAL47094'1; EMEL; AF400623; AAL47094'1; JOINED. EMEL; AF400624; AAL47094'1; JOINED. EMEL; AF400625; AAL47094'1; JOINED. EMEL; AF400627; AAL47094'1; JOINED. EMEL; AF400627; AAL47094'1; JOINED. EMEL; AF400629; AAL47094'1; JOINED. EMEL; AF400629; AAL47094'1; JOINED. EMEL; AC029386; AAL47094'1; JOINED. EMEL; AC029386; AAL47094'1; JOINED. EMEL; AC02933; GGDEW; HGNC'8104; OCLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1258; OCCLUDIN.
Coiled coil; Phosphorylation;
DOMAIN 1 66
C
CRANGMEM 67 89 P
DOMAIN 90 135 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U49184; AAC50451.1; -. EMBL; U53823; AAB00195.1; -.
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TRANSMEM
DOMAIN
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A MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Zeeberg B.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Bardwas S.I., Wang J., Hsieh F., Datchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L., Scheefer B. B., Bonaldo M.F., Casavant T.L., Scheefer T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., A., Romas S.A., McEwan P.J., McKernan K.J., Malamy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malamy S.J., Bosak S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulton E., Ketteman M., Madan A.M., Rodrigues S., Sanchez M., Mating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M. Maray M.M., Green E.D., Dickson M.C., Ratingue S., Schmutz J., Myers R.M., Butterfield Y.S., Anches S.J., Marra M.A.;
Jones S.J., Marra M.A.;
M. Green E.D., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.;
M. Green E.D., Schmutz J., Myers R.M., Butterfield W. Green E.D., Dickson M.C., Green E.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
M. Green E.D., Schutz J., Myers R.M., Butterfield W. Green E.D., Dickson M.C., Green E.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
M. Green E.D., Schutz J., Specker E.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
M. Proc. Natl. Acad. Sci. U.S.A., 99:16699-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                               80.9%; Score 106; DB 1; Length 522; 91.7%; Pred. No. 3.6e-06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 106; DB 2; Length 523; 91.7%; Pred. No. 3.6e-06; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. .
TISSUE=Prostate;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
   244 265 Potential.
266 522 Cytoplasmic (Potential).
92 131 TYR/GLY-RICH.
93 Colled coil (Potential).
233 233 L -> S (in Ref. 4).
522 AA, 59143 MM, AOCF9574BCF6E974 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 3 REESEEYMAAADEYNRLKQVKQPA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                   468 REESEEYMAAADEYNRLKOVKGSA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BC062037, AAH62037.1, -.
InterPro, IPR008253, Marvel.
InterPro, IPR002558, Occludin.
InterPro, IPR010844; Occludin_ELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01284; MARVEL; 1.
Pfam; PF07303; Occludin_ELL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                  Local Similarity 91.7%;
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.74
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate;
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05-JUL-2004 (
05-JUL-2004 (
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TRANSMEM
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DOMAIN
CONFLICT
SEQUENCE
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Matches
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3 REESEEYMAAADEYNRLKQVKQPA 26

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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=OCLN;
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Q28269;
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OCLN_CANFA
      SORENERE
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A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hesteh F.,

A Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Poters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabersley S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabersley W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodiguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                    karlus norvegique (kat).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    katuus norvegicus (kat).
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=SD; TISSUE=Liver;
Kokai Y., Kuwahara K., Atsumi S., Mori M.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO15625; BAA36681.1; -..
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 AA; 59214 MW; SEIE007568AEA5B1 CRC64;
                                                                                                                                                                                                                         Created)
Last sequence update)
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Last sequence update)
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                                                                                                                                                               523 AA.
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469 REESEEYMAAADEYNRLKQVKGSA 492
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                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR008253; Marvel.
InterPro, IPR002958; Occludin.
InterPro, IPR010844; Occludin_ELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 REESEEYMAAADEYNRLKQVKQPA
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Pfam; PF07303; Occludin ELL; 1.
PRINTS; PR01258; OCCLUDIN.
SEQUENCE 523 AA; 59214 MM·····
                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAX-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
22; Conserve
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Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.;
"Possible involvement of phosphorylation of occludin in tight junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- FUNCTION: May play a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier. Interacts with ZO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Interacts with VAPA (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.
-!- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Necessary for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction (By similarity).
-!- PTM: Phosphorylated. Less-phosphorylated forms are found in basolateral membrane, cytosol and tight junction. More-heavily phosphorylated forms are concentrated exclusively in tight
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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BIGLINE=96181088; PubMed=8601611;
Ando-Akateuka Y., Saltou M., Hirase T., Kishi M., Sakakibara A.,
Itoh M., Yonemura S., Furuse M., Tsukita S.;
Innerspecies diversity of the occludin sequence: cDNA cloning of huma., mouse, dog, and rat-kangaroo homologues.";
J. Cell Biol. 133:43-47(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                         Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

80.9%; Score 106; DB 2; Length 52
Best Local Similarity 91.7%; Pred. No. 3.6e-06;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               ALSOLDER R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ database=
EMBL; BC062037; AAH62037.1; -. A31E007BS9AEASBS CRC64;
SROTENCE 523 AA; 59186 MW; A31E007BS9AEASBS CRC64;
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Name=OCLN;
                                                                                  Occludin.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=20143583; PubMed=10679019; MEDINE=20143583; PubMed=10679019; Muresan Z., Paul D.L., Goodenough D.A.; Moccludin.1B, a variant of the tight junction protein occludin."; Mol. Biol. Cell 11:627-634 (2000). EMBL; AF246976; AAF62172.1; -.. EMBL; AF246976; AAF62172.1; -.. EMBL; AF208053; Marvel. InterPro; IPR008253; Marvel. InterPro; IPR008253; Marvel. InterPro; IPR008553; Marvel. InterPro; IPR008554; Occludin.
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                                                                                                                                                                                                   Tight junction, Transmembrane.
Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
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2875E59F8F0AlFFA CRC64;
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Potential.
Cytoplasmic (Potential).
TYR/GLY-RICH.
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Cytoplasmic (Potential).
Potential.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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EMBL, U49221, AAC48582.1; -.
InterPro; IPR008253; Marvel.
InterPro; IPR002958; Occludin.
InterPro; IPR010844; Occludin_ELL.
Pfem; PP01284; MARVEL; 1.
Pfem; PF07303; Occludin_ELL; 1.
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Pfam; PF07303; Occludin ELL; 1.
PRINTS; PR01258; OCCLUDIN.
                                                                                                                                                                       PRINTS; PRO1258; OCCLUDIN.
Coiled coil; Phosphorylation; T.
DOMAIN 1 66 CY
TRANSMEM 67 89 POI
DOMAIN 90 134 EXI
TRANSMEM 135 159 POI
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AC Q9PUN1;
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493 AA.

PRT;

STANDARD;

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Cordenonsi M., Mazzon E., De Rigo L., Baraldo S., Meggio F., Citi S.,
Cordenonsi M., Mazzon E., De Rigo L., Baraldo S., Meggio F., Citi S.,
Cordenonsi M., Mazzon E., De Rigo L., Baraldo S., Meggio F., Citi S.,
Cordenonsi M., Mazzon E., De Rigo L., Baraldo S., Meggio F., Citi S.,
Cordenonsi M., Mazzon E., De Rigo L., Baraldo S., Meggio F., Citi S.,
Cordi Sci. 110:1313-13139(1997).
Cordenonsi M., Mazzon E., De Rigo L., Cordenonsi Regulation of the tight junction (TJ) paracellular permeability barrier.
Cordenonsi Interacts in vitro with cingulin, possibly directly.
Cordenonsi M. Merchalla C. (198 similarity).
Cordenonsi M. Merchalla C. (198 similarity).
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                                                                                                                                                                                                                                                                                                                                              MEDIINE=99421641; PubMed=10491082;
Cordenonsi M., Turco F., D'Atri F., Hammar E., Martinucci G.,
Meggio F., Citi S.;
"Xenopus laevis occludin. Identification of in vitro phosphorylation
sites by protein kinase CK2 and association with cingulin.";
Eur. J. Blochem. 264:374-384 (1999).
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES THR-375 AND SER-379
                                                                                                                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etages.
--- DOMAIN: The C-terminus is cytoplasmic and is important for interaction with ZO-1. Necessary for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction (By similarity).
--- PTM: Phosphorylated.
--- SIMILARITY: Belongs to the ELL / occludin family.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleosto
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Colled coil; Phosphorylation, Tight junction, Transmembrane.
Colled coil; 1
1 TRANSMEM 48 70 Potential.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                    Xenopus laevis (African clawed frog)
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InterPro; IPR002958; Occludin.
InterPro; IPR010844; Occludin_ELL.
Pfam; PF01284; MARVEL, 1.
Pfam; PF07303; Occludin_ELL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=98034414; PubMed=9365283;
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